



Gly Leu Asn Asp

FIG. 4



TGGCCTGCAC	CCCACCCCC	AGCCTGCGAA	GACGGGGGA	GGCGGTGGTC	GGTCGCCTCC	60
CTCCTGCCCC	CGGCCTGGCT	TCGCGGTGGA	GGCGGTGCCT	CTCCGGCAAG	GCAGACCAGG	120
CTGGGCGGAC	GCGCGGCGCG	GGGCGGGCTA	GGGAAGGCCG	GGGGCCTCGC	GCTCGGGCCC	180
CGGGCGGCGA	CTGACAGCGG	CGGCGGCGGC	GGCAGCGGCT	CCAAGGCGAG	CGTGGTCCCC	240
GCGTGCGCAC	AAGCTCGCCG	CCGCGCAGGG	ACCCACGGAC	ACCGGCGCCG	GGCGGACACA	300
CAGACGCGGA	GATCGGGCTC	TACGCGCGCT	ACTCAGCGCA	CGAGCTCCCC	ATCCCTGGGC	360
GGAGCGGGGC	GCGGACTCGC	CGCTGCGCGC	CCTCCCCGCG	GAGTCTGCCC	CGGGCAGACC	420
CGCAGCCCGC	GGCCCCGCCG	CGAGGCCCT	GGGTGAGCAG	CCTGTAGACA	GCTGGGGTTG	480
AGCAGTGGCG	GCTGTGA	ATG AGA GGC GGG CGG CAC	TGG CCC GAG CCG CCT			530
		Met Arg Gly Gly Arg His	Trp Pro Glu Pro Pro			
	1		5		10	

TGC AGG CTG AGA AGC GTC ATG GCC AGC ATC GCG CAG GTC TCC CTG GCT	578
Cys Arg Leu Arg Ser Val Met Ala Ser Ile Ala Gln Val Ser Leu Ala	
	15 20 25

GCT CTC CTC CTG CTG CCT ATG GCC ACC GCC ATG CAT TCC GAC TGC ATC	626
Ala Leu Leu Leu Leu Pro Met Ala Thr Ala Met His Ser Asp Cys Ile	
	30 35 40

TTC AAG AAG GAG CAA GCC ATG TGC CTG GAG AAG ATC CAG AGG GTG AAT	674
Phe Lys Lys Glu Gln Ala Met Cys Leu Glu Lys Ile Gln Arg Val Asn	
	45 50 55

GAC CTG ATG GGC TTG AAT GAC TCC TCC CCA GGG TGC CCT GGG ATG TGG	722
Asp Leu Met Gly Leu Asn Asp Ser Ser Pro Gly Cys Pro Gly Met Trp	
	60 65 70 75

GAC AAC ATC ACG TGT TGG AAG CCC GCC CAC GTG GGT GAG ATG GTC CTG	770
Asp Asn Ile Thr Cys Trp Lys Pro Ala His Val Gly Glu Met Val Leu	
	80 85 90

GTC AGT TGC CCT GAA CTC TTC CGA ATC TTC AAC CCA GAC CAA GTC TGG	818
Val Ser Cys Pro Glu Leu Phe Arg Ile Phe Asn Pro Asp Gln Val Trp	
	95 100 105

GAG ACG GAA ACC ATC GGA GAG TTC GGT TTT GCA GAC AGT AAA TCC TTG	866
Glu Thr Glu Thr Ile Gly Glu Phe Gly Phe Ala Asp Ser Lys Ser Leu	
	110 115 120

GAT CTC TCA GAC ATG AGG GTG GTG AGC CGG AAT TGC ACG GAG GAT GGA	914
Asp Leu Ser Asp Met Arg Val Val Ser Arg Asn Cys Thr Glu Asp Gly	
	125 130 135

TGG TCA GAG CCA TTC CCT CAT TAT TTC GAT GCC TGT GGG TTT GAG GAG	962
Trp Ser Glu Pro Phe Pro His Tyr Phe Asp Ala Cys Gly Phe Glu Glu	
	140 145 150 155

TAC GAA TCT GAG ACT GGG GAC CAG GAT TAC TAC TAC CTG TCA GTG AAG	1010
Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr Tyr Tyr Leu Ser Val Lys	
	160 165 170

FIG. 2A

GCC	CTG	TAC	ACA	GTT	GGC	TAC	AGC	ACG	TCC	CTC	GTC	ACC	CTC	ACC	ACT	1058
Ala	Leu	Tyr	Thr	Val	Gly	Tyr	Ser	Thr	Ser	Leu	Val	Thr	Leu	Thr	Thr	
			175					180							185	
GCC	ATG	GTC	ATC	CTG	TGT	CGT	TTC	CGG	AAG	CTG	CAC	TGC	ACC	CGC	AAC	1106
Ala	Met	Val	Ile	Leu	Cys	Arg	Phe	Arg	Lys	Leu	His	Cys	Thr	Arg	Asn	
		190					195					200				
TTC	ATC	CAC	ATG	AAC	CTC	TTC	GTG	TCG	TTT	ATG	CTG	AGG	GCC	ATC	TCC	1154
Phe	Ile	His	Met	Asn	Leu	Phe	Val	Ser	Phe	Met	Leu	Arg	Ala	Ile	Ser	
	205					210					215					
GTC	TTC	ATC	AAA	GAC	TGG	ATC	CTC	TAT	GCT	GAG	CAG	GAC	AGC	AAT	CAC	1202
Val	Phe	Ile	Lys	Asp	Trp	Ile	Leu	Tyr	Ala	Glu	Gln	Asp	Ser	Asn	His	
	220				225					230					235	
TGC	TTT	GTC	TCC	ACT	GTG	GAA	TGC	AAG	GCT	GTG	ATG	GTT	TTC	TTC	CAC	1250
Cys	Phe	Val	Ser	Thr	Val	Glu	Cys	Lys	Ala	Val	Met	Val	Phe	Phe	His	
				240					245					250		
TAC	TGT	GTT	GTA	TCC	AAC	TAC	TTC	TGG	CTG	TTC	ATC	GAG	GGC	CTG	TAT	1298
Tyr	Cys	Val	Val	Ser	Asn	Tyr	Phe	Trp	Leu	Phe	Ile	Glu	Gly	Leu	Tyr	
			255					260					265			
CTC	TTC	ACC	CTG	CTG	GTG	GAG	ACC	TTC	TTC	CCC	GAG	AGG	AGA	TAT	TTC	1346
Leu	Phe	Thr	Leu	Leu	Val	Glu	Thr	Phe	Phe	Pro	Glu	Arg	Arg	Tyr	Phe	
		270					275					280				
TAC	TGG	TAC	ATC	ATC	ATT	GGC	TGG	GGG	ACA	CCA	ACT	GTG	TGT	GTG	TCT	1394
Tyr	Trp	Tyr	Ile	Ile	Ile	Gly	Trp	Gly	Thr	Pro	Thr	Val	Cys	Val	Ser	
	285					290					295					
GTG	TGG	GCT	ATG	CTG	AGG	CTC	TAC	TTC	GAT	GAC	ACA	GGC	TGC	TGG	GAT	1442
Val	Trp	Ala	Met	Leu	Arg	Leu	Tyr	Phe	Asp	Asp	Thr	Gly	Cys	Trp	Asp	
	300				305			310						315		
ATG	AAT	GAC	AAC	ACG	GCT	CTG	TGG	TGG	GTG	ATC	AAA	GGC	CCT	GTA	GTT	1490
Met	Asn	Asp	Asn	Thr	Ala	Leu	Trp	Trp	Val	Ile	Lys	Gly	Pro	Val	Val	
				320				325						330		
GGC	TCC	ATA	ATG	GTT	AAT	TTT	GTG	CTC	TTC	ATC	GGC	ATC	ATT	GTC	ATC	1538
Gly	Ser	Ile	Met	Val	Asn	Phe	Val	Leu	Phe	Ile	Gly	Ile	Ile	Val	Ile	
			335				340						345			
CTT	GTG	CAG	AAA	CTT	CAG	TCT	CCA	GAC	ATG	GGA	GGC	AAC	GAG	TCC	AGC	1586
Leu	Val	Gln	Lys	Leu	Gln	Ser	Pro	Asp	Met	Gly	Gly	Asn	Glu	Ser	Ser	
		350					355					360				
ATC	TAC	TTC	AGC	TGC	GTG	CAG	AAA	TGC	TAC	TGC	AAG	CCA	CAG	CGG	GCT	1634
Ile	Tyr	Phe	Ser	Cys	Val	Gln	Lys	Cys	Tyr	Cys	Lys	Pro	Gln	Arg	Ala	
	365					370					375					
CAG	CAG	CAC	TCT	TGC	AAG	ATG	TCA	GAA	CTG	TCC	ACC	ATT	ACT	CTA	CGG	1682
Gln	Gln	His	Ser	Cys	Lys	Met	Ser	Glu	Leu	Ser	Thr	Ile	Thr	Leu	Arg	

FIG. 2B

380	385	390	395	
CTC GCC AGG TCC ACC TTG CTG CTC ATC CCA CTC TTT GGA ATC CAC TAC				1730
Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile His Tyr	400	405	410	
ACT GTC TTT GCT TTC TCC CCG GAG AAC GTC AGC AAG AGG GAG AGA CTG				1778
Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys Arg Glu Arg Leu	415	420	425	
GTG TTT GAG CTG GGT CTG GGC TCC TTC CAG GGC TTT GTG GTG GCT GTT				1826
Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val Ala Val	430	435	440	
CTC TAT TGC TTT CTG AAT GGA GAG GTG CAG GCG GAG ATC AAG AGG AAG				1874
Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu Ile Lys Arg Lys	445	450	455	
TGG CGG AGC TGG AAG GTG AAC CGC TAC TTC ACC ATG GAC TTC AAG CAC				1922
Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe Thr Met Asp Phe Lys His	460	465	470	475
CGG CAC CCA TCC CTG GCC AGC AGC GGG GTG AAC GGG GGC ACC CAG CTC				1970
Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly Gly Thr Gln Leu	480	485	490	
TCC ATC CTG AGC AAG AGC AGC TCC CAG ATC CGC ATG TCT GGG CTT CCG				2018
Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met Ser Gly Leu Pro	495	500	505	
GCC GAC AAC CTG GCC ACC TGAGCCCACC CTGCCCCCTC CTCTCCTCTG TACGCAGGC				2075
Ala Asp Asn Leu Ala Thr	510			
TGGGGCTGTG GTGGGGCGCC GGCCACGCA TGTGTGCTT CTTCTCGCCT TCGGGCAGGC				2135
CCCGGGCTGG GCGCCTGGCC CCCGAGGTTG GAGAAGGATG CGGGACAGGC AGCTGTTTAG				2195
CCTTCCTGTT TTGGCGCTGG CCCAACCACC GTGGGTCCCT GGGCCTGCAC CCAGACATGT				2255
AATACTCCTT AATTGGGAAG TCATCCATTC TTTCCCTTTT CCAAGTCCTT GCTTATTAAG				2315
AGGTTCAAGT CACCTACCCA ATTCAGAAGC TTAAGTAACC ACTAACCACC GTGACTGCGT				2375
GGGAGGCCTC CCATGGGCTG AGCTACTGAC TTGGCTTTGG GGGCCTTGGG CTGGGGCCCT				2435
CCTTAAAGCC CCCCTTGAAA TTGTCGGACC TCAAAGTGTG ACTCCTTTGA GTCTACTCGC				2495
CACCCCGTG GCCCTTTGCA GCCCTGGTCC AGTCACCGAG GTTACTGGAA GTCCAGCTTG				2555
GATGGCCAGA CAGCTTTTTG GCACAGGCAG ACCCATGCTC ACCCAACATT TTAGTGTCCA				2615
GGTGCCCAGG TGCCCAGGTG CCCAGCTCCT GGGCATCAGA CAGTGGGAAA GCTCCAGGGA				2675
TCTACCATTG AGAGACTTCA GTTTGGATGT AGGGCTAAGG CCAGAGAAAA GTTCTGGAGC				2735
TTTTCATTTG GCCCAAGAAA AAAGTCCAA GATCCAGAAA AGTGGATCTG AGTGAATTT				2795
AGATGCAAAG AGCTTGGAG				2814

FIG. 2C

TGGCCTGCAC	CCCACCCCC	AGCCTGCGAA	GACGGGGGGA	GGCGGTGGTC	GGTCGCCTCC	60
CTCCTGCCCC	CGGCCTGGCT	TCGCGGTGGA	GGCGGTGCCT	CTCCGGCAAG	GCAGACCAGG	120
CTGGGCGGAC	GCGCGGCGCG	GGGCGGGCTA	GGGAAGGCCG	GGGGCCTCGC	GCTCGGGCCC	180
CGGGCGGCGA	CTGACAGCGG	CGGCGGCGGC	GGCAGCGGCT	CCAAGGCGAG	CGTGGTCCCC	240
GCGTGCGCAC	AAGCTCGCCG	CCGCGCAGGG	ACCCACGGAC	ACCGGCGCCG	GGCGGACACA	300
CAGACGCGGA	GATCGGGCTC	TACGCGCGCT	ACTCAGCGCA	CGAGCTCCCC	ATCCCTGGGC	360
GGAGCGGGGC	GCGGACTCGC	CGCTGCGCGC	CCTCCCCGCG	GAGTCTGCC	CGGGCAGACC	420
CGCAGCCCGC	GGCCCCGCCG	CGAGGCCCT	GGGTGAGCAG	CCTGTAGACA	CCTGGGGTTG	480
AGCAGTGGCG	GCTGTGA	ATG AGA GGC GGG CGG CAC	TGG CCC GAG	CCG CCT		530

Met Arg Gly Gly Arg His Trp Pro Glu Pro Pro  
1 5 10

TGC AGG CTG AGA AGC GTC ATG GCC AGC ATC GCG CAG GTC TCC CTG GCT	578
Cys Arg Leu Arg Ser Val Met Ala Ser Ile Ala Gln Val Ser Leu Ala	
15 20 25	

GCT CTC CTC CTG CTG CCT ATG GCC ACC GCC ATG CAT TCC GAC TGC ATC	626
Ala Leu Leu Leu Leu Pro Met Ala Thr Ala Met His Ser Asp Cys Ile	
30 35 Δ 40	

TTC AAG AAG GAG CAA GCC ATG TGC CTG GAG AAG ATC CAG AGG GTG AAT	674
Phe Lys Lys Glu Gln Ala Met Cys Leu Glu Lys Ile Gln Arg Val Asn	
45 50 55	

GAC CTG ATG GGC TTG AAT GAC TCC TCC CCA GGG TGC CCT GGG ATG TGG	722
Asp Leu Met Gly Leu Asn Asp Ser Ser Pro Gly Cys Pro Gly Met Trp	
60 65 70 75	

GAC AAC ATC ACG TGT TGG AAG CCC GCC CAC GTG GGT GAG ATG GTC CTG	770
Asp Asn Ile Thr Cys Trp Lys Pro Ala His Val Gly Glu Met Val Leu	
80 85 90	

GTC AGT TGC CCT GAA CTC TTC CGA ATC TTC AAC CCA GAC CAA GTC TGG	818
Val Ser Cys Pro Glu Leu Phe Arg Ile Phe Asn Pro Asp Gln Val Trp	
95 100 105	

GAG ACG GAA ACC ATC GGA GAG TTC GGT TTT GCA GAC AGT AAA TCC TTG	866
Glu Thr Glu Thr Ile Gly Glu Phe Gly Phe Ala Asp Ser Lys Ser Leu	
110 115 120	

GAT CTC TCA GAC ATG AGG GTG GTG AGC CGG AAT TGC ACG GAG GAT GGA	914
Asp Leu Ser Asp Met Arg Val Val Ser Arg Asn Cys Thr Glu Asp Gly	
125 130 135	

TGG TCA GAG CCA TTC CCT CAT TAT TTC GAT GCC TGT GGG TTT GAG GAG	962
Trp Ser Glu Pro Phe Pro His Tyr Phe Asp Ala Cys Gly Phe Glu Glu	
140 145 150 155	

TAC GAA TCT GAG ACT GGG GAC CAG GAT TAC TAC TAC CTG TCA GTG AAG	1010
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FIG. 3A

Tyr	Glu	Ser	Glu	Thr	Gly	Asp	Gln	Asp	Tyr	Tyr	Tyr	Leu	Ser	Val	Lys	
				160					165					170		
GCC	CTG	TAC	ACA	GTT	GGC	TAC	AGC	ACG	TCC	CTC	GTC	ACC	CTC	ACC	ACT	1058
Ala	Leu	Tyr	Thr	Val	Gly	Tyr	Ser	Thr	Ser	Leu	Val	Thr	Leu	Thr	Thr	
			175					180					185			
GCC	ATG	GTC	ATC	CTG	TGT	CGT	TTC	CGG	AAG	CTG	CAC	TGC	ACC	CGC	AAC	1106
Ala	Met	Val	Ile	Leu	Cys	Arg	Phe	Arg	Lys	Leu	His	Cys	Thr	Arg	Asn	
		190					195					200				
TTC	ATC	CAC	ATG	AAC	CTC	TTC	GTG	TCG	TTT	ATG	CTG	AGG	GCC	ATC	TCC	1154
Phe	Ile	His	Met	Asn	Leu	Phe	Val	Ser	Phe	Met	Leu	Arg	Ala	Ile	Ser	
	205					210					215					
GTC	TTC	ATC	AAA	GAC	TGG	ATC	CTC	TAT	GCT	GAG	CAG	GAC	AGC	AAT	CAC	1202
Val	Phe	Ile	Lys	Asp	Trp	Ile	Leu	Tyr	Ala	Glu	Gln	Asp	Ser	Asn	His	
	220				225					230					235	
TGC	TTT	GTC	TCC	ACT	GTG	GAA	TGC	AAG	GCT	GTG	ATG	GTT	TTC	TTC	CAC	1250
Cys	Phe	Val	Ser	Thr	Val	Glu	Cys	Lys	Ala	Val	Met	Val	Phe	Phe	His	
				240				245						250		
TAC	TGT	GTT	GTA	TCC	AAC	TAC	TTC	TGG	CTG	TTC	ATC	GAG	GGC	CTG	TAT	1298
Tyr	Cys	Val	Val	Ser	Asn	Tyr	Phe	Trp	Leu	Phe	Ile	Glu	Gly	Leu	Tyr	
			255					260					265			
CTC	TTC	ACC	CTG	CTG	GTG	GAG	ACC	TTC	TTC	CCC	GAG	AGG	AGA	TAT	TTC	1346
Leu	Phe	Thr	Leu	Leu	Val	Glu	Thr	Phe	Phe	Pro	Glu	Arg	Arg	Tyr	Phe	
		270					275					280				
TAC	TGG	TAC	ATC	ATC	ATT	GGC	TGG	GGG	ACA	CCA	ACT	GTG	TGT	GTG	TCT	1394
Tyr	Trp	Tyr	Ile	Ile	Ile	Gly	Trp	Gly	Thr	Pro	Thr	Val	Cys	Val	Ser	
	285					290					295					
GTG	TGG	GCT	ATG	CTG	AGG	CTC	TAC	TTC	GAT	GAC	ACA	GGC	TGC	TGG	GAT	1442
Val	Trp	Ala	Met	Leu	Arg	Leu	Tyr	Phe	Asp	Asp	Thr	Gly	Cys	Trp	Asp	
	300				305					310					315	
ATG	AAT	GAC	AAC	ACG	GCT	CTG	TGG	TGG	GTG	ATC	AAA	GGC	CCT	GTA	GTT	1490
Met	Asn	Asp	Asn	Thr	Ala	Leu	Trp	Trp	Val	Ile	Lys	Gly	Pro	Val	Val	
				320					325					330		
GGC	TCC	ATA	ATG	GTT	AAT	TTT	GTG	CTC	TTC	ATC	GGC	ATC	ATT	GTC	ATC	1538
Gly	Ser	Ile	Met	Val	Asn	Phe	Val	Leu	Phe	Ile	Gly	Ile	Ile	Val	Ile	
			335					340					345			
CTT	GTG	CAG	AAA	CTT	CAG	TCT	CCA	GAC	ATG	GGA	GGC	AAC	GAG	TCC	AGC	1586
Leu	Val	Gln	Lys	Leu	Gln	Ser	Pro	Asp	Met	Gly	Gly	Asn	Glu	Ser	Ser	
		350					355					360				
ATC	TAC	TTA	CGG	CTC	GCC	AGG	TCC	ACC	TTG	CTG	CTC	ATC	CCA	CTC	TTT	1634
Ile	Tyr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu	Leu	Leu	Ile	Pro	Leu	Phe	
	365					370					375					

FIG. 3B

GGA ATC CAC TAC ACT GTC TTT GCT TTC TCC CCG GAG AAC GTC AGC AAG 1682  
 Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys  
 380 385 390 395

AGG GAG AGA CTG GTG TTT GAG CTG GGT CTG GGC TCC TTC CAG GGC TTT 1730  
 Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe  
 400 405 410

GTG GTG GCT GTT CTC TAT TGC TTT CTG AAT GGA GAG GTG CAG GCG GAG 1778  
 Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu  
 415 420 425

ATC AAG AGG AAG TGG CGG AGC TGG AAG GTG AAC CGC TAC TTC ACC ATG 1826  
 Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe Thr Met  
 430 435 440

GAC TTC AAG CAC CGG CAC CCA TCC CTG GCC AGC AGC GGG GTG AAC GGG 1874  
 Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly  
 445 450 455

GGC ACC CAG CTC TCC ATC CTG AGC AAG AGC AGC TCC CAG ATC CGC ATG 1922  
 Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met  
 460 465 470 475

TCT GGG CTT CCG GCC GAC AAC CTG GCC ACC TGAGCCCACC CTGCCCCCTC CTCT 1976  
 Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr  
 480 485

CCTCTGTACG	CAGGCTGGGG	CTGTGGTGGG	GCGCCGGCCC	ACGCATGTTG	TGCCTCTTCT	2036
CGCCTTCGGG	CAGGCCCCGG	GCTGGGCGCC	TGGCCCCGA	GGTTGGAGAA	GGATGCGGGA	2096
CAGGCAGCTG	TTTAGCCTTC	CTGTTTTGGC	GCTGGCCCAA	CCACCGTGGG	TCCCTGGGCC	2156
TGCACCCAGA	CATGTAATAC	TCCTTAATTG	GGAAGTCATC	CATTCTTTCC	CTTTCCCAAG	2216
TCCTTGCTTA	TTAAGAGGTT	CAAGTCACCT	ACCCAATTCA	GAAGCTTAAG	TAACCACTAA	2276
CCACCGTGAC	TGCGTGGGAG	GCCTCCCATG	GGCTGAGCTA	CTGACTTGGC	TTTGGGGGCC	2336
TTGGGCTGGG	GCCCTCCTTA	AAGCCCCCCC	TGAAATTGTC	GGACCTCAAA	GTGTGACTCC	2396
TTTGAGTCTA	CTCGCCACCC	CCGTGGCCCT	TTGCAGCCCT	GGTCCAGTCA	CCGAGGTTAC	2456
TGGAAGTCCA	GCTTGATGG	CCAGACAGCT	TTTTGGCACA	GGCAGACCCA	TGCTCACCCA	2516
ACATTTTAGT	GTCCAGGTGC	CCAGGTGCCC	AGGTGCCCAG	CTCCTGGGCA	TCAGACAGTG	2576
GGAAAGCTCC	AGGGATCTAC	CATTCAGAGA	CTTCAGTTTG	GATGTAGGGC	TAAGGCCAGA	2636
GAAAAGTTCT	GGAGCTTTTC	ATTTGGCCCA	AGAAAAAACT	GCCAAGATCC	AGAAAAGTGG	2696
ATCTGAGTGG	AATTTAGATG	CAAAGAGCTT	GGAG			2730

FIG. 3C





CGAGTGGACA GTGGCAGGCG GTGACTGAAT CTCCAAGTCT GGAAACAATA GCCAGAGATA	60
GTGGCTGGGA AGCACC ATG GCC AGA GTC CTG CAG CTC TCC CTG ACT GCT CTC	112
Met Ala Arg Val Leu Gln Leu Ser Leu Thr Ala Leu	
1 5 10	
CTG CTG CCT GTG GCT ATT GCT ATG CAC TCT GAC TGC ATC TTC AAG AAG	160
Leu Leu Pro Val Ala Ile Ala Met His Ser Asp Cys Ile Phe Lys Lys	
15 20 25	
GAG CAA GCC ATG TGC CTG GAG AGG ATC CAG AGG GCC AAC GAC CTG ATG	208
Glu Gln Ala Met Cys Leu Glu Arg Ile Gln Arg Ala Asn Asp Leu Met	
30 35 40	
GGA CTA AAC GAG TCT TCC CCA GGT TGC CCT GGC ATG TGG GAC AAT ATC	256
Gly Leu Asn Glu Ser Ser Pro Gly Cys Pro Gly Met Trp Asp Asn Ile	
45 50 55 60	
ACA TGT TGG AAG CCA GCT CAA GTA GGT GAG ATG GTC CTT GTA AGC TGC	304
Thr Cys Trp Lys Pro Ala Gln Val Gly Glu Met Val Leu Val Ser Cys	
65 70 75	
CCT GAG GTC TTC CGG ATC TTC AAC CCG GAC CAA GTC TGG ATG ACA GAA	352
Pro Glu Val Phe Arg Ile Phe Asn Pro Asp Gln Val Trp Met Thr Glu	
80 85 90	
ACC ATA GGA GAT TCT GGT TTT GCC GAT AGT AAT TCC TTG GAG ATC ACA	400
Thr Ile Gly Asp Ser Gly Phe Ala Asp Ser Asn Ser Leu Glu Ile Thr	
95 100 105	
GAC ATG GGG GTC GTG GGC CGG AAC TGC ACA GAG GAC GGC TGG TCG GAG	448
Asp Met Gly Val Val Gly Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu	
110 115 120	
CCC TTC CCC CAC TAC TTC GAT GCT TGT GGG TTT GAT GAT TAT GAG CCT	496
Pro Phe Pro His Tyr Phe Asp Ala Cys Gly Phe Asp Asp Tyr Glu Pro	
125 130 135 140	
GAG TCT GGA GAT CAG GAT TAT TAC TAC CTG TCG GTG AAG GCT CTC TAC	544
Glu Ser Gly Asp Gln Asp Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr	
145 150 155	
ACA GTC GGC TAC AGC ACT TCC CTC GCC ACC CTC ACT ACT GCC ATG GTC	592
Thr Val Gly Tyr Ser Thr Ser Leu Ala Thr Leu Thr Thr Ala Met Val	
160 165 170	
ATC TTG TGC CGC TTC CGG AAG CTG CAT TGC ACT CGC AAC TTC ATC CAC	640
Ile Leu Cys Arg Phe Arg Lys Leu His Cys Thr Arg Asn Phe Ile His	
175 180 185	
ATG AAC CTG TTT GTA TCC TTC ATG CTG AGG GCT ATC TCC GTC TTC ATC	688
Met Asn Leu Phe Val Ser Phe Met Leu Arg Ala Ile Ser Val Phe Ile	

FIG. 7A

190	195	200	
AAG GAC TGG ATC TTG TAC GCC GAG CAG GAC AGC AGT CAC TGC TTC GTT Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp Ser Ser His Cys Phe Val 205 210 215 220	736		
TCC ACC GTG GAG TGC AAA GCT GTC ATG GTT TTC TTC CAC TAC TGC GTG Ser Thr Val Glu Cys Lys Ala Val Met Val Phe Phe His Tyr Cys Val 225 230 235	784		
GTG TCC AAC TAC TTC TGG CTG TTC ATT GAA GGC CTG TAC CTC TTT ACA Val Ser Asn Tyr Phe Trp Leu Phe Ile Glu Gly Leu Tyr Leu Phe Thr 240 245 250	832		
CTG CTG GTG GAG ACC TTC TTC CCT GAG AGG AGA TAT TTC TAC TGG TAC Leu Leu Val Glu Thr Phe Phe Pro Glu Arg Arg Tyr Phe Tyr Trp Tyr 255 260 265	880		
ACC ATC ATC GGC TGG GGG ACA CCT ACT GTG TGT GTA ACA GTG TGG GCT Thr Ile Ile Gly Trp Gly Thr Pro Thr Val Cys Val Thr Val Trp Ala 270 275 280	928		
GTG CTG AGG CTC TAT TTT GAT GAT GCA GGA TGC TGG GAT ATG AAT GAC Val Leu Arg Leu Tyr Phe Asp Asp Ala Gly Cys Trp Asp Met Asn Asp 285 290 295 300	976		
AGC ACA GCT CTG TGG TGG GTG ATC AAA GGC CCC GTG GTT GGC TCT ATA Ser Thr Ala Leu Trp Trp Val Ile Lys Gly Pro Val Val Gly Ser Ile 305 310 315	1024		
ATG GTT AAC TTT GTG CTT TTC ATC GGC ATC ATC ATC ATC CTT GTA CAG Met Val Asn Phe Val Leu Phe Ile Gly Ile Ile Ile Ile Leu Val Gln 320 325 330	1072		
AAG CTG CAG TCC CCA GAC ATG GGA GGC AAC GAG TCC AGC ATC TAC TTA Lys Leu Gln Ser Pro Asp Met Gly Gly Asn Glu Ser Ser Ile Tyr Leu 335 340 345	1120		
CGG CTG GCC CGC TCC ACC CTA CTG CTC ATC CCA CTC TTC GGA ATC CAC Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile His 350 355 360	1168		
TAC ACA GTA TTC GCC TTC TCT CCA GAG AAC GTC AGC AAG AGG GAA AGA Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys Arg Glu Arg 365 370 375 380	1216		
CTT GTG TTT GAG CTT GGG CTG GGC TCC TTC CAG GGC TTT GTG GTG GCT Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val Ala 385 390 395	1264		
GTA CTC TAC TGC TTC CTG AAT GGG GAG GTA CAG GCA GAG ATT AAG AGG Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu Ile Lys Arg 400 405 410	1312		

FIG. 7B

AAA TGG AGG AGC TGG AAG GTG AAC CGT TAC TTC ACT ATG GAC TTC AAG 1360  
 Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe Thr Met Asp Phe Lys  
 415 420 425

CAC CGG CAC CCG TCC CTG GCC AGC AGT GGA GTA AAT GGG GGA ACC CAG 1408  
 His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly Gly Thr Gln  
 430 435 440

CTG TCC ATC CTG AGC AAG AGC AGC TCC CAG CTC CGC ATG TCC AGC CTC 1456  
 Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Leu Arg Met Ser Ser Leu  
 445 450 455 460

CCG GCC GAC AAC TTG GCC ACC TGAGGCCTGT CTCCTCCTC CTTCTGCACA GGCTG 1512  
 Pro Ala Asp Asn Leu Ala Thr \*\*\*  
 465

GGGCTGCGGG CCAGTGCCTG AGCATGTTTG TGCCTCTCCC CTCTCCTTGG GCAGGCCCTG 1572  
 GGTAGGAAGC TGGGCTCCTC CCCAAAGGGG AAGAGAGAGA TAGGGTATAG GCTGATATTG 1632  
 CTCCTCCTGT TTGGGTCCCA CCTACTGTGA TTCATTGAGC CTGATTTGAC ATGTAAATAC 1692  
 ACCTCAAATT TGGAAAGTTG CCCCATCTCT GCCCCCAACC CATGCCCTG CTCACCTCTG 1752  
 CCAGGCCCCA GCTCAACCTA CTGTGTCAAG GCCAGCCTCA GTGATAGTCT GATCCCAGGT 1812  
 ACAAGGCCTT GTGAGCTGAG GCTGAAAGGC CTGTTTTGGA GAGGCTGGGG TAGTGCC 1869

FIG. 8

CGAGTGGACA GTGGCAGGCG GTGACTGAAT CTCCAAGTCT GGAAACAATA GCCAGAGATA	60
GTGGCTGGGA AGCACC ATG GCC AGA GTC CTG CAG CTC TCC CTG ACT GCT CTC	112
Met Ala Arg Val Leu Gln Leu Ser Leu Thr Ala Leu	
1 5 10	
CTG CTG CCT GTG GCT ATT GCT ATG CAC TCT GAC TGC ATC TTC AAG AAG	160
Leu Leu Pro Val Ala Ile Ala Met His Ser Asp Cys Ile Phe Lys Lys	
15 $\Delta$ 20 25	
GAG CAA GCC ATG TGC CTG GAG AGG ATC CAG AGG GCC AAC GAC CTG ATG	208
Glu Gln Ala Met Cys Leu Glu Arg Ile Gln Arg Ala Asn Asp Leu Met	
30 35 40	
GGA CTA AAC GAG TCT TCC CCA GGT TGC CCT GGC ATG TGG GAC AAT ATC	256
Gly Leu Asn Glu Ser Ser Pro Gly Cys Pro Gly Met Trp Asp Asn Ile	
45 50 55 60	
ACA TGT TGG AAG CCA GCT CAA GTA GGT GAG ATG GTC CTT GTA AGC TGC	304
Thr Cys Trp Lys Pro Ala Gln Val Gly Glu Met Val Leu Val Ser Cys	
65 70 75	
CCT GAG GTC TTC CGG ATC TTC AAC CCG GAC CAA GTC TGG ATG ACA GAA	352
Pro Glu Val Phe Arg Ile Phe Asn Pro Asp Gln Val Trp Met Thr Glu	
80 85 90	
ACC ATA GGA GAT TCT GGT TTT GCC GAT AGT AAT TCC TTG GAG ATC ACA	400
Thr Ile Gly Asp Ser Gly Phe Ala Asp Ser Asn Ser Leu Glu Ile Thr	
95 100 105	
GAC ATG GGG GTC GTG GGC CGG AAC TGC ACA GAG GAC GGC TGG TCG GAG	448
Asp Met Gly Val Val Gly Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu	
110 115 120	
CCC TTC CCC CAC TAC TTC GAT GCT TGT GGG TTT GAT GAT TAT GAG CCT	496
Pro Phe Pro His Tyr Phe Asp Ala Cys Gly Phe Asp Asp Tyr Glu Pro	
125 130 135 140	
GAG TCT GGA GAT CAG GAT TAT TAC TAC CTG TCG GTG AAG GCT CTC TAC	544
Glu Ser Gly Asp Gln Asp Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr	
145 150 155	
ACA GTC GGC TAC AGC ACT TCC CTC GCC ACC CTC ACT ACT GCC ATG GTC	592
Thr Val Gly Tyr Ser Thr Ser Leu Ala Thr Leu Thr Thr Ala Met Val	
160 165 170	
ATC TTG TGC CGC TTC CGG AAG CTG CAT TGC ACT CGC AAC TTC ATC CAC	640
Ile Leu Cys Arg Phe Arg Lys Leu His Cys Thr Arg Asn Phe Ile His	
175 180 185	
ATG AAC CTG TTT GTA TCC TTC ATG CTG AGG GCT ATC TCC GTC TTC ATC	688
Met Asn Leu Phe Val Ser Phe Met Leu Arg Ala Ile Ser Val Phe Ile	
190 195 200	

FIG. 9A

AAG Lys 205	GAC Asp	TGG Trp	ATC Ile	TTG Leu	TAC Tyr 210	GCC Ala	GAG Glu	CAG Gln	GAC Asp 215	AGC Ser	AGT Ser	CAC His	TGC Cys	TTC Phe	GTT Val 220	736
TCC Ser	ACC Thr	GTG Val	GAG Glu	TGC Cys 225	AAA Lys	GCT Ala	GTC Val	ATG Met	GTT Val 230	TTC Phe	TTC Phe	CAC His	TAC Tyr	TGC Cys 235	GTG Val	784
GTG Val	TCC Ser	AAC Asn	TAC Tyr 240	TTC Phe	TGG Trp	CTG Leu	TTC Phe	ATT Ile 245	GAA Glu	GGC Gly	CTG Leu	TAC Tyr	CTC Leu 250	TTT Phe	ACA Thr	832
CTG Leu	CTG Leu	GTG Val 255	GAG Glu	ACC Thr	TTC Phe	TTC Phe	CCT Pro 260	GAG Glu	AGG Arg	AGA Arg	TAT Tyr	TTC Phe 265	TAC Tyr	TGG Trp	TAC Tyr	880
ACC Thr 270	ATC Ile	ATC Ile	GGC Gly	TGG Trp	GGG Gly	ACA Thr 275	CCT Pro	ACT Thr	GTG Val	TGT Cys	GTA Val 280	ACA Thr	GTG Val	TGG Trp	GCT Ala	928
GTG Val 285	CTG Leu	AGG Arg	CTC Leu	TAT Tyr	TTT Phe 290	GAT Asp	GAT Asp	GCA Ala	GGG Gly	TGC Cys 295	TGG Trp	GAT Asp	ATG Met	AAT Asn	GAC Asp 300	976
AGC Ser	ACA Thr	GCT Ala	CTG Leu	TGG Trp 305	TGG Trp	GTG Val	ATC Ile	AAA Lys	GGC Gly 310	CCC Pro	GTG Val	GTT Val	GGC Gly	TCT Ser 315	ATA Ile	1024
ATG Met	GTT Val	AAC Asn	TTT Phe 320	GTG Val	CTT Leu	TTC Phe	ATC Ile	GGC Gly 325	ATC Ile	ATC Ile	ATC Ile	ATC Ile	CTT Leu 330	GTA Val	CAG Gln	1072
AAG Lys	CTG Leu	CAG Gln 335	TCC Ser	CCA Pro	GAC Asp	ATG Met	GGA Gly 340	GGC Gly	AAC Asn	GAG Glu	TCC Ser	AGC Ser 345	ATC Ile	TAC Tyr	TTC Phe Δ	1120
AGC Ser 350	TGC Cys	GTG Val	CAG Gln	AAA Lys	TGC Cys	TAC Tyr 355	TGC Cys	AAG Lys	CCA Pro	CAG Gln	CGG Arg 360	GCT Ala	CAG Gln	CAG Gln	CAC His	1168
TCT Ser 365	TGC Cys	AAG Lys	ATG Met	TCA Ser	GAA Glu 370	CTA Leu	TCC Ser	ACC Thr	ATT Ile	ACT Thr 375	CTA Leu Δ	CGG Arg	CTG Leu	GCC Ala	CGC Arg 380	1216
TCC Ser	ACC Thr	CTA Leu	CTG Leu	CTC Leu 385	ATC Ile	CCA Pro	CTC Leu	TTC Phe	GGA Gly 390	ATC Ile	CAC His	TAC Tyr	ACA Thr	GTA Val 395	TTC Phe	1264
GCC Ala	TTC Phe	TCT Ser	CCA Pro 400	GAG Glu	AAC Asn	GTC Val	AGC Ser	AAG Lys 405	AGG Arg	GAA Glu	AGA Arg	CTT Leu	GTG Val 410	TTT Phe	GAG Glu	1312
CTT Leu	GGG Gly	CTG Leu	GGC Gly	TCC Ser	TTC Phe	CAG Gln	GGC Gly	TTT Phe	GTG Val	GTG Val	GCT Ala	GTA Val	CTC Leu	TAC Tyr	TGC Cys	1360

FIG. 9B

415	420	425	
TTC CTG AAT GGG GAG GTA CAG GCA GAG ATT AAG AGG AAA TGG AGG AGC Phe Leu Asn Gly Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser 430 435 440			1408
TGG AAG GTG AAC CGT TAC TTC ACT ATG GAC TTC AAG CAC CGG CAC CCG Trp Lys Val Asn Arg Tyr Phe Thr Met Asp Phe Lys His Arg His Pro 445 450 455 460			1456
TCC CTG GCC AGC AGT GGA GTA AAT GGG GGA ACC CAG CTG TCC ATC CTG Ser Leu Ala Ser Ser Gly Val Asn Gly Gly Thr Gln Leu Ser Ile Leu 465 470 475			1504
AGC AAG AGC AGC TCC CAG CTC CGC ATG TCC AGC CTC CCG GCC GAC AAC Ser Lys Ser Ser Ser Gln Leu Arg Met Ser Ser Leu Pro Ala Asp Asn 480 485 490			1552
TTG GCC ACC TGAGGCCTGT CTCCCTCCTC CTTCTGCACA GGCTGGGGCT GCGGGCCAGT Leu Ala Thr 495			1611
GCCTGAGCAT GTTTGTGCCT CTCCCCTCTC CTTGGGCAGG CCCTGGGTAG GAAGCTGGGC TCCTCCCCAA AGGGGAAGAG AGAGATAGGG TATAGGCTGA TATTGCTCCT CCTGTTTGGG TCCCACCTAC TGTGATTCAT TGAGCCTGAT TTGACATGTA AATACACCTC AAATTTGGAA AGTTGCCCCA TCTCTGCCCC CAACCCATGC CCCTGCTCAC CTCTGCCAGG CCCCAGCTCA ACCTACTGTG TCAAGGCCAG CCTCAGTGAT AGTCTGATCC CAGGTACAAG GCCTTGTGAG CTGAGGCTGA AAGGCCTGTT TTGGAGAGGC TGGGGTAGTG CCCACCCCAG CAGCCTTTCA GCAAATTGAC TTTGGATGTG GACCCTTCTC AGCCTGTACC AAGTACTGCA GTTGGCTAGG GATGCAGCTC AGTTTCCTGA GCATCCTTTG GAGCAGGTCA ACCTGAGGCT CCTTTTGCTT ACCCGACATC TAAGTTGTCC AGGTGCTCGG CTCCTGTGTG CCTGGATGAC GGGAGGGCTC CGGGGTCTTT CAGTCAAAGA CTTACATTGA GGTGGGGTGA GAGTCAGAGA AAAGTTCTGG TGCTTTTCAT TTGTTCTAAG AGCTGAGAGC CAGGAATGCA GAGTCAATTG GGAAGGAGAT GGGATAGCTG ATGATCTTAC CATGTCCATG ACTGTGCCCC TGATTCAAGA CCGGATCATG TGGTGGCTTT ATTTCTACAC TTCTTGTCCA CAATGGACAG TCTGAGGAAG CTCTTCTTTC AGCCACAACA ACCACAGAAA GCCCTTTCTT CTCCCCTCTT GTTTCTCCAT AAGTCAAAGC CATGTTTAGA ACGGACCAGC CACCTTGCGA TGAAATCACT GAGTTCTGAA GCAACTTTCA ATTTCCACGA GCCAAGTCCT GGGTCCAGGG ACGCCCC			1671 1731 1791 1851 1911 1971 2031 2091 2151 2211 2271 2331 2391 2451 2511 2548

FIG. 10

Rat Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu  
 \* \* \* \* \*

Bovine Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu  
 1 5 10 15

Rat Arg Ile Gln Arg Ala Asn Asp Leu Met Gly Leu Asn Glu  
 \* \* \* \* \*

Bovine Lys Ile Gln Arg Val Asn Asp Leu Met Gly Leu Asn Asp  
 20 25

FIG. 11

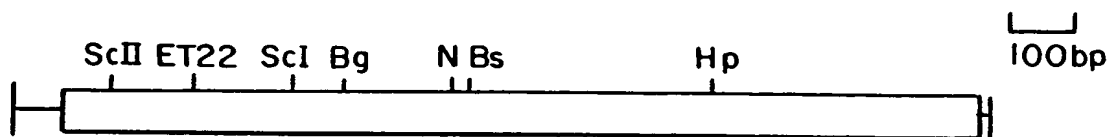


FIG. 12

Human Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu  
 5 10 15  
 \* \* \* \* \*

Bovine Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu

Human Gly Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp  
 20 25  
 \* \* \* \* \*

Bovine Glu Lys Ile Gln Arg Val Asn Asp Leu Met Gly Leu Asn Asp

FIG. 14

AGCCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGCTG	60
GCCAAGAAGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT GCT CAC	109
Met Ala Gly Val Val His Val Ser Leu Ala Ala His	
1 5 10	
TGC GGG GCC TGT CCG TGG GGC CGG GGC AGA CTC CGC AAA GGA CGC GCA	157
Cys Gly Ala Cys Pro Trp Gly Arg Gly Arg Leu Arg Lys Gly Arg Ala	
15 20 25	
GCC TGC AAG TCC GCG GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG	205
Ala Cys Lys Ser Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu	
30 35 40	
CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA AGT GTC ATG GCT GGT	253
Leu Ser Val Gly Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly	
45 50 55 60	
GTC GTG CAC GTT TCC CTG GCT GCT CTC CTC CTG CTG CCT ATG GCC CCT	301
Val Val His Val Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Pro	
65 70 75	
GCC ATG CAT TCT GAC TGC ATC TTC AAG AAG GAG CAA GCC ATG TGC CTG	349
Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu	
80 85 90	
GAG AAG ATC CAG AGG GCC AAT GAG CTG ATG GGC TTC AAT GAT TCC TCT	397
Glu Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser	
95 100 105	
CCA GGC TGT CCT GGG ATG TGG GAC AAC ATC ACG TGT TGG AAG CCC GCC	445
Pro Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala	
110 115 120	
CAT GTG GGT GAG ATG GTC CTG GTC AGC TGC CCT GAG CTC TTC CGA ATC	493
His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile	
125 130 135 140	
TTC AAC CCA GAC CAA GTC TGG GAG ACC GAA ACC ATT GGA GAG TCT GAT	541
Phe Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp	
145 150 155	
TTT GGT GAC AGT AAC TCC TTA GAT CTC TCA GAC ATG GGA GTG GTG AGC	589
Phe Gly Asp Ser Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser	
160 165 170	
CGG AAC TGC ACG GAG GAT GGC TGG TCG GAA CCC TTC CCT CAT TAC TTT	637
Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe	
175 180 185	
GAT GCC TGT GGG TTT GAT GAA TAT GAA TCT GAG ACT GGG GAC CAG GAT	685
Asp Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp	

FIG. 13A



190	195	200	
TAT Tyr 205	TAC Tyr	TAC Tyr	CTG Leu
TCA Ser	GTG Val 210	AAG Lys	GCC Ala
CTC Leu	TAC Tyr	ACG Thr 215	GTT Val
GGC Gly	TAC Tyr	AGC Ser	ACA Thr 220
733			
TCC Ser	CTC Leu	GTC Val 230	ATC Ile
CTT Leu	TGT Cys	CGC Arg	TTC Phe 235
CGG Arg			
781			
AAG Lys	CTG Leu	CAC His	TGC Cys 240
ACA Thr	CGC Arg	AAC Asn	TTC Phe 245
ATC Ile 245	CAC His	ATG Met	AAC Asn
CTG Leu	TTT Phe 250	GTG Val	TCG Ser
829			
TTC Phe	ATG Met	CTG Leu 255	AGG Arg
GCG Ala	ATC Ile	TCC Ser	GTC Val 260
TTC Phe	ATC Ile	AAA Lys	GAC Asp 265
TGG Trp 265	ATT Ile	CTG Leu	TAT Tyr
877			
GCG Ala 270	GAG Glu	CAG Gln	GAC Asp
AGC Ser	AAC Asn	CAC His 275	TGC Cys
TTC Phe	ATC Ile	TCC Ser	ACT Thr 280
GTG Val	GAA Glu	TGT Cys	AAG Lys
925			
GCC Ala 285	GTC Val	ATG Met	GTT Val
TTC Phe	TTC Phe 290	CAC His	TAC Tyr
TGT Cys	GTT Val 295	GTG Val	TCC Ser
AAC Asn	TAC Tyr	TTC Phe	TTC Phe 300
973			
CTG Leu	TTC Phe	ATC Ile	GAG Glu
GGC Gly 305	CTG Leu	TAC Tyr	CTC Leu
TTC Phe	ACT Thr 310	CTG Leu	CTG Leu
GTG Val	GAG Glu 315	ACC Thr	TTC Phe
1021			
TTC Phe	CCT Pro	GAA Glu	AGG Arg 320
AGA Arg	TAC Tyr	TTC Phe	TAC Tyr
TGG Trp 325	TAC Tyr	ACC Thr	ATC Ile
ATT Ile	GGC Gly 330	TGG Trp	GGG Gly
1069			
TCC Ser	CCA Pro	ACT Thr 335	GTG Val
TGT Cys	GTG Val	ACA Thr	GTG Val 340
TGG Trp	GCT Ala	ACG Thr	CTG Leu
AGA Arg 345	CTC Leu	TAC Tyr	TTT Phe
1117			
GAT Asp 350	GAC Asp	ACA Thr 350	GCT Ala
CTG Leu	TGG Trp	TGG Trp	
1165			
GTG Val 365	ATC Ile	AAA Lys	GGC Gly
CCT Pro	GTG Val 370	GTT Val	GGC Gly
TCT Ser	ATC Ile 375	ATG Met	GTT Val
AAC Asn	TTT Phe	GTG Val 380	CTT Leu
1213			
TTT Phe	ATT Ile	GGC Gly	ATT Ile
ATC Ile 385	GTC Val	ATC Ile	CTT Leu
GTG Val	CAG Gln 390	AAA Lys	CTT Leu
CAG Gln	TCT Ser	CCA Pro 395	GAC Asp
1261			
ATG Met	GGA Gly	GGC Gly	AAT Asn 400
GAG Glu	TCC Ser	AGC Ser	ATC Ile 405
TAC Tyr 405	TTG Leu	CGA Arg	CTG Leu
GCC Ala	CGG Arg 410	TCC Ser	ACC Thr
1309			

FIG. 13B

CTG	CTG	CTC	ATC	CCA	CTA	TTC	GGA	ATC	CAC	TAC	ACA	GTA	TTT	GCC	TTC	1357
Leu	Leu	Leu	Ile	Pro	Leu	Phe	Gly	Ile	His	Tyr	Thr	Val	Phe	Ala	Phe	
		415					420					425				
TCC	CCA	GAG	AAT	GTC	AGC	AAA	AGG	GAA	AGA	CTC	GTG	TTT	GAG	CTG	GGG	1405
Ser	Pro	Glu	Asn	Val	Ser	Lys	Arg	Glu	Arg	Leu	Val	Phe	Glu	Leu	Gly	
	430					435					440					
CTG	GGC	TCC	TTC	CAG	GGC	TTT	GTG	GTG	GCT	GTT	CTC	TAC	TGT	TTT	CTG	1453
Leu	Gly	Ser	Phe	Gln	Gly	Phe	Val	Val	Ala	Val	Leu	Tyr	Cys	Phe	Leu	
445					450					455					460	
AAT	GGT	GAG	GTA	CAA	GCG	GAG	ATC	AAG	CGA	AAA	TGG	CGA	AGC	TGG	AAG	1501
Asn	Gly	Glu	Val	Gln	Ala	Glu	Ile	Lys	Arg	Lys	Trp	Arg	Ser	Trp	Lys	
				465					470					475		
GTG	AAC	CGT	TAC	TTC	GCT	GTG	GAC	TTC	AAG	CAC	CGA	CAC	CCG	TCT	CTG	1549
Val	Asn	Arg	Tyr	Phe	Ala	Val	Asp	Phe	Lys	His	Arg	His	Pro	Ser	Leu	
			480					485					490			
GCC	AGC	AGT	GGG	GTG	AAT	GGG	GGC	ACC	CAG	CTC	TCC	ATC	CTG	AGC	AAG	1597
Ala	Ser	Ser	Gly	Val	Asn	Gly	Gly	Thr	Gln	Leu	Ser	Ile	Leu	Ser	Lys	
		495					500					505				
AGC	AGC	TCC	CAA	ATC	CGC	ATG	TCT	GGC	CTC	CCT	GCT	GAC	AAT	CTG	GCC	1645
Ser	Ser	Ser	Gln	Ile	Arg	Met	Ser	Gly	Leu	Pro	Ala	Asp	Asn	Leu	Ala	
	510					515					520					
ACC	TGAGCCATGC	TCCCCT														1664
Thr																
525																

FIG. 13C

Rat	Asn	Glu	Ser	Ser	Ile	Tyr	Phe	Ser	Cys	Val	Gln	Lys	Cys	Tyr	Cys	Lys
Type I-B	AAC	GAG	TCC	AGC	ATC	TAC	TTC	AGC	TGC	GTG	CAG	AAA	TGC	TAC	TGC	AAA

pHRP15A	Asn	Glu	Ser	Ser	Ile	Tyr	Phe	Ser	Cys	Val	Gln	Lys	Cys	Tyr	Cys	Lys
human Type I-B	AAT	GAG	TCC	AGC	ATC	TAC	TTC	AGC	TGC	GTG	CAG	AAA	TGC	TAC	TGC	AAG

pHRP55A	Asn	Glu	Ser	Ser	Ile	Tyr	Phe	—	Cys	Val	Gln	Lys	Cys	Tyr	Cys	Lys
Type I-B2	AAT	GAG	TCC	AGC	ATC	TAC	TTC		TGC	GTG	CAG	AAA	TGC	TAC	TGC	AAG

pHRP66P	Asn	Glu	Ser	Ser	Ile	Tyr	Leu	Thr	Asn	Leu	Ser	Pro	Arg	Val	Pro	Lys
Type I-C	AAT	GAG	TCC	AGC	ATC	TAC	TTA	ACA	AAT	TTA	AGC	CCG	CGA	GTC	CCC	AAG

Pro	Gln	Arg	Ala	Gln	Gln	His	Ser	Cys	Lys	Met	Ser	Glu	Leu	Ser	Thr
CCA	CAG	CGG	CGT	CAG	CAG	CAC	TCT	TGC	AAG	ATC	TCA	GAA	CTA	TCC	ACC

Pro	Gln	Arg	Ala	Gln	Gln	His	Ser	Cys	Lys	Met	Ser	Glu	Leu	Ser	Thr
CCA	CAG	CGG	GCT	CAG	CAG	CAC	TCT	TGC	AAG	ATG	TCA	GAA	CTG	TCC	ACC

Pro	Gln	Arg	Ala	Gln	Gln	His	Ser	Cys	Lys	Met	Ser	Glu	Leu	Ser	Thr
CCA	CAG	CGG	GCT	CAG	CAG	CAC	TCT	TGC	AAG	ATG	TCA	GAA	CTG	TCC	ACC

Lys	Ala	Arg	Glu	Asp	Pro	Leu	Pro	Val	Pro	Ser	Asp	Gln	His	Ser	Leu
AAA	GCC	CGA	GAG	GAC	CCC	CTG	CCT	GTG	CCC	TCA	GAC	CAG	CAT	TCA	CTC

Ile	Thr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu
ATT	ACT	CTA	CGG	CTG	GCC	CGC	TCC	ACC	CTA

Ile	Thr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu
ATT	ACT	CTG	CGA	CTG	GCC	CGG	TCC	ACC	CTG

Ile	Thr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu
ATT	ACT	CTG	CGA	CTG	GCC	CGG	TCC	ACC	CTG

Pro	Phe	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu
CCT	TTC	CTG	CGA	CTG	GCC	CGG	TCC	ACC	CTG

FIG. 15

AGCCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGCTG	60
GCCAAGAAGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT GCT CAC	109
Met Ala Gly Val Val His Val Ser Leu Ala Ala His	
1 5 10	
TGC GGG GCC TGT CCG TGG GGC CGG GGC AGA CTC CGC AAA GGA CGC GCA	157
Cys Gly Ala Cys Pro Trp Gly Arg Gly Arg Leu Arg Lys Gly Arg Ala	
15 20 25	
GCC TGC AAG TCC GCG GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG	205
Ala Cys Lys Ser Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu	
30 35 40	
CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA AGT GTC ATG GCT GGT	253
Leu Ser Val Gly Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly	
45 50 55 60	
GTC GTG CAC GTT TCC CTG GCT GCT CTC CTC CTG CTG CCT ATG GCC CCT	301
Val Val His Val Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Pro	
65 70 75	
GCC ATG CAT TCT GAC TGC ATC TTC AAG AAG GAG CAA GCC ATG TGC CTG	349
Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu	
80 85 90	
GAG AAG ATC CAG AGG GCC AAT GAG CTG ATG GGC TTC AAT GAT TCC TCT	397
Glu Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser	
95 100 105	
CCA GGC TGT CCT GGG ATG TGG GAC AAC ATC ACG TGT TGG AAG CCC GCC	445
Pro Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala	
110 115 120	
CAT GTG GGT GAG ATG GTC CTG GTC AGC TGC CCT GAG CTC TTC CGA ATC	493
His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile	
125 130 135 140	
TTC AAC CCA GAC CAA GTC TGG GAG ACC GAA ACC ATT GGA GAG TCT GAT	541
Phe Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp	
145 150 155	
TTT GGT GAC AGT AAC TCC TTA GAT CTC TCA GAC ATG GGA GTG GTG AGC	589
Phe Gly Asp Ser Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser	
160 165 170	
CGG AAC TGC ACG GAG GAT GGC TGG TCG GAA CCC TTC CCT CAT TAC TTT	637
Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe	
175 180 185	
GAT GCC TGT GGG TTT GAT GAA TAT GAA TCT GAG ACT GGG GAC CAG GAT	685
Asp Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp	

FIG. 16A

190	195	200	
TAT Tyr 205	TAC Tyr	TAC Tyr	CTG Leu
TCA Ser	GTG Val 210	AAG Lys	GCC Ala
CTC Leu	TAC Tyr	ACG Thr 215	GTT Val
GGC Gly	TAC Tyr	AGC Ser	ACA Thr 220
733			
TCC Ser	CTC Leu	GTC Val 230	ATC Ile
CTT Leu	TGT Cys	CGC Arg	TTC Phe 235
CGG Arg	781		
AAG Lys	CTG Leu	CAC His	TGC Cys 240
ACA Thr	CGC Arg	AAC Asn	TTC Phe 245
ATC Ile	CAC His	ATG Met	AAC Asn
CTG Leu	TTT Phe 250	GTG Val	TCG Ser
829			
TTC Phe	ATG Met	CTG Leu	AGG Arg 255
GCG Ala	ATC Ile	TCC Ser	GTG Val 260
TTC Phe	ATC Ile	AAA Lys	GAC Asp 265
TGG Trp	ATT Ile	CTG Leu	TAT Tyr
877			
GCG Ala	GAG Glu 270	CAG Gln	GAC Asp
AGC Ser	AAC Asn	CAC His 275	TGC Cys
TTC Phe	ATC Ile	TCC Ser	ACT Thr 280
GTG Val	GAA Glu	TGT Cys	AAG Lys
925			
GCC Ala 285	GTG Val	ATG Met	GTT Val
TTC Phe	TTC Phe 290	CAC His	TAC Tyr
TGT Cys	GTT Val 295	GTG Val	TCC Ser
AAC Asn	TAC Tyr	TTC Phe	TGG Trp 300
973			
CTG Leu	TTC Phe	ATC Ile	GAG Glu 305
GGC Gly	CTG Leu	TAC Tyr	CTC Leu
TTC Phe	ACT Thr 310	CTG Leu	CTG Leu
GTG Val	GAG Glu 315	ACC Thr	TTC Phe
1021			
TTC Phe	CCT Pro	GAA Glu	AGG Arg 320
AGA Arg	TAC Tyr	TTC Phe	TAC Tyr
TGG Trp 325	TAC Tyr	ACC Thr	ATC Ile
ATT Ile	GGC Gly 330	TGG Trp	GGG Gly
1069			
ACC Thr	CCA Pro	ACT Thr 335	GTG Val
TGT Cys	GTG Val	ACA Thr	GTG Val 340
TGG Trp	GCT Ala	ACG Thr	CTG Leu
AGA Arg 345	CTC Leu	TAC Tyr	TTT Phe
1117			
GAT Asp	GAC Asp 350	ACA Thr	GGC Gly
TGC Cys	TGG Trp	GAT Asp 355	ATG Met
AAT Asn	GAC Asp	AGC Ser	ACA Thr 360
GCT Ala	CTG Leu	TGG Trp	TGG Trp
1165			
GTG Val 365	ATC Ile	AAA Lys	GGC Gly
CCT Pro	GTG Val 370	GTT Val	GGC Gly
TCT Ser	ATC Ile	ATG Met 375	GTT Val
AAC Asn	TTT Phe	GTG Val 380	CTT Leu
1213			
TTT Phe	ATT Ile	GGC Gly	ATT Ile
ATC Ile 385	GTC Val	ATC Ile	CTT Leu
GTG Val	CAG Gln 390	AAA Lys	CTT Leu
CAG Gln	TCT Ser	CCA Pro 395	GAC Asp
1261			
ATG Met	GGA Gly	GGC Gly	AAT Asn 400
GAG Glu	TCC Ser	AGC Ser	ATC Ile 405
TAC Tyr	TTC Phe	AGC Ser	TGC Cys
GTG Val	CAG Gln 410	AAA Lys	TGC Cys
1309			

FIG. 16B

TAC TGC AAG CCA CAG CGG GCT CAG CAG CAC TCT TGC AAG ATG TCA GAA 1357  
 Tyr Cys Lys Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu  
 415 420 425

CTG TCC ACC ATT ACT CTG CGA CTG GCC CGG TCC ACC CTG CTG CTC ATC 1405  
 Leu Ser Thr Ile Thr Leu Arg Leu, Ala Arg Ser Thr Leu Leu Leu Ile  
 430 435 440

CCA CTA TTC GGA ATC CAC TAC ACA GTA TTT GCC TTC TCC CCA GAG AAT 1453  
 Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn  
 445 450 455 460

GTC AGC AAA AGG GAA AGA CTC GTG TTT GAG CTG GGG CTG GGC TCC TTC 1501  
 Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe  
 465 470 475

CAG GGC TTT GTG GTG GCT GTT CTC TAC TGT TTT CTG AAT GGT GAG GTA 1549  
 Gln Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val  
 480 485 490

CAA GCG GAG ATC AAG CGA AAA TGG CGA AGC TGG AAG GTG AAC CGT TAC 1597  
 Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr  
 495 500 505

TTC GCT GTG GAC TTC AAG CAC CGA CAC CCG TCT CTG GCC AGC AGT GGG 1645  
 Phe Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly  
 510 515 520

GTG AAT GGG GGC ACC CAG CTC TCC ATC CTG AGC AAG AGC AGC TCC CAA 1693  
 Val Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln  
 525 530 535 540

ATC CGC ATG TCT GGC CTC CCT GCT GAC AAT CTG GCC ACC TGAGCCATGC TCC 1745  
 Ile Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr  
 545 550

CCT 1748

F I G. 16C

AGCCCAGAGA	CACATTGGGG	CTGACCTGCC	GCTGCTGTCA	GTGGGAGGCC	AGTGGTGCTG	60										
GCCAAGAAGT	GTC	ATG	GCT	GGT	GTC	GTG	CAC	GTT	TCC	CTG	GCT	GCT	CAC	109		
	1	Met	Ala	Gly	Val	Val	His	Val	Ser	Leu	Ala	Ala	His			
						5							10			
TGC	GGG	GCC	TGT	CCG	TGG	GGC	CGG	GGC	AGA	CTC	CGC	AAA	GGA	CGC	GCA	157
Cys	Gly	Ala	Cys	Pro	Trp	Gly	Arg	Gly	Arg	Leu	Arg	Lys	Gly	Arg	Ala	
	15						20					25				
GCC	TGC	AAG	TCC	GCG	GCC	CAG	AGA	CAC	ATT	GGG	GCT	GAC	CTG	CCG	CTG	205
Ala	Cys	Lys	Ser	Ala	Ala	Gln	Arg	His	Ile	Gly	Ala	Asp	Leu	Pro	Leu	
	30					35					40					
CTG	TCA	GTG	GGA	GGC	CAG	TGG	TGC	TGG	CCA	AGA	AGT	GTC	ATG	GCT	GGT	253
Leu	Ser	Val	Gly	Gly	Gln	Trp	Cys	Trp	Pro	Arg	Ser	Val	Met	Ala	Gly	
	45				50					55					60	
GTC	GTG	CAC	GTT	TCC	CTG	GCT	GCT	CTC	CTC	CTG	CTG	CCT	ATG	GCC	CCT	301
Val	Val	His	Val	Ser	Leu	Ala	Ala	Leu	Leu	Leu	Leu	Pro	Met	Ala	Pro	
				65					70					75		
GCC	ATG	CAT	TCT	GAC	TGC	ATC	TTC	AAG	AAG	GAG	CAA	GCC	ATG	TGC	CTG	349
Ala	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	
			80					85				90				
GAG	AAG	ATC	CAG	AGG	GCC	AAT	GAG	CTG	ATG	GGC	TTC	AAT	GAT	TCC	TCT	397
Glu	Lys	Ile	Gln	Arg	Ala	Asn	Glu	Leu	Met	Gly	Phe	Asn	Asp	Ser	Ser	
	95						100					105				
CCA	GGC	TGT	CCT	GGG	ATG	TGG	GAC	AAC	ATC	ACG	TGT	TGG	AAG	CCC	GCC	445
Pro	Gly	Cys	Pro	Gly	Met	Trp	Asp	Asn	Ile	Thr	Cys	Trp	Lys	Pro	Ala	
	110					115					120					
CAT	GTG	GGT	GAG	ATG	GTC	CTG	GTC	AGC	TGC	CCT	GAG	CTC	TTC	CGA	ATC	493
His	Val	Gly	Glu	Met	Val	Leu	Val	Ser	Cys	Pro	Glu	Leu	Phe	Arg	Ile	
	125				130					135					140	
TTC	AAC	CCA	GAC	CAA	GTC	TGG	GAG	ACC	GAA	ACC	ATT	GGA	GAG	TCT	GAT	541
Phe	Asn	Pro	Asp	Gln	Val	Trp	Glu	Thr	Glu	Thr	Ile	Gly	Glu	Ser	Asp	
				145					150					155		
TTT	GGT	GAC	AGT	AAC	TCC	TTA	GAT	CTC	TCA	GAC	ATG	GGA	GTG	GTG	AGC	589
Phe	Gly	Asp	Ser	Asn	Ser	Leu	Asp	Leu	Ser	Asp	Met	Gly	Val	Val	Ser	
			160					165					170			
CGG	AAC	TGC	ACG	GAG	GAT	GGC	TGG	TCG	GAA	CCC	TTC	CCT	CAT	TAC	TTT	637
Arg	Asn	Cys	Thr	Glu	Asp	Gly	Trp	Ser	Glu	Pro	Phe	Pro	His	Tyr	Phe	
	175						180					185				
GAT	GCC	TGT	GGG	TTT	GAT	GAA	TAT	GAA	TCT	GAG	ACT	GGG	GAC	CAG	GAT	685
Asp	Ala	Cys	Gly	Phe	Asp	Glu	Tyr	Glu	Ser	Glu	Thr	Gly	Asp	Gln	Asp	
	190					195					200					

FIG. 17A

TAT Tyr 205	TAC Tyr	TAC Tyr	CTG Leu	TCA Ser	GTG Val 210	AAG Lys	GCC Ala	CTC Leu	TAC Tyr	ACG Thr 215	GTT Val	GGC Gly	TAC Tyr	AGC Ser	ACA Thr 220	733
TCC Ser	CTC Leu	GTC Val	ACC Thr	CTC Leu 225	ACC Thr	ACT Thr	GCC Ala	ATG Met	GTC Val 230	ATC Ile	CTT Leu	TGT Cys	CGC Arg	TTC Phe	CGG Arg 235	781
AAG Lys	CTG Leu	CAC His	TGC Cys 240	ACA Thr	CGC Arg	AAC Asn	TTC Phe	ATC Ile 245	CAC His	ATG Met	AAC Asn	CTG Leu	TTT Phe 250	GTG Val	TCG Ser	829
TTC Phe	ATG Met	CTG Leu 255	AGG Arg	GCG Ala	ATC Ile	TCC Ser	GTC Val 260	TTC Phe	ATC Ile	AAA Lys	GAC Asp	TGG Trp 265	ATT Ile	CTG Leu	TAT Tyr	877
GCG Ala 270	GAG Glu	CAG Gln	GAC Asp	AGC Ser	AAC Asn	CAC His 275	TGC Cys	TTC Phe	ATC Ile	TCC Ser	ACT Thr 280	GTG Val	GAA Glu	TGT Cys	AAG Lys	925
GCC Ala 285	GTC Val	ATG Met	GTT Val	TTC Phe 290	TTC Phe	CAC His	TAC Tyr	TGT Cys	GTT Val 295	GTG Val	TCC Ser	AAC Asn	TAC Tyr	TTC Phe	TGG Trp 300	973
CTG Leu	TTC Phe	ATC Ile	GAG Glu 305	GGC Gly	CTG Leu	TAC Tyr	CTC Leu	TTC Phe	ACT Thr 310	CTG Leu	CTG Leu	GTG Val	GAG Glu	ACC Thr 315	TTC Phe	1021
TTC Phe	CCT Pro	GAA Glu	AGG Arg 320	AGA Arg	TAC Tyr	TTC Phe	TAC Tyr	TGG Trp 325	TAC Tyr	ACC Thr	ATC Ile	ATT Ile	GGC Gly 330	TGG Trp	GGG Gly	1069
ACC Thr	CCA Pro	ACT Thr 335	GTG Val	TGT Cys	GTG Val	ACA Thr 340	GTG Val	TGG Trp	GCT Ala	ACG Thr	CTG Leu	AGA Arg 345	CTC Leu	TAC Tyr	TTT Phe	1117
GAT Asp 350	GAC Asp	ACA Thr	GGC Gly	TGC Cys	TGG Trp	GAT Asp 355	ATG Met	AAT Asn	GAC Asp	AGC Ser	ACA Thr 360	GCT Ala	CTG Leu	TGG Trp	TGG Trp	1165
GTG Val 365	ATC Ile	AAA Lys	GGC Gly	CCT Pro	GTG Val 370	GTT Val	GGC Gly	TCT Ser	ATC Ile	ATG Met 375	GTT Val	AAC Asn	TTT Phe	GTG Val 380	CTT Leu	1213
TTT Phe	ATT Ile	GGC Gly	ATT Ile	ATC Ile 385	GTC Val	ATC Ile	CTT Leu	GTG Val	CAG Gln 390	AAA Lys	CTT Leu	CAG Gln	TCT Ser	CCA Pro	GAC Asp 395	1261
ATG Met	GGA Gly	GGC Gly	AAT Asn 400	GAG Glu	TCC Ser	AGC Ser	ATC Ile	TAC Tyr 405	TTC Phe	TGC Cys	GTG Val	CAG Gln	AAA Lys 410	TGC Cys	TAC Tyr	1309
TGC Cys	AAG Lys	CCA Pro	CAG Gln	CGG Arg	GCT Ala	CAG Gln	CAG Gln	CAC His	TCT Ser	TGC Cys	AAG Lys	ATG Met	TCA Ser	GAA Glu	CTG Leu	1357

FIG. 17B



415					420					425										
TCC	ACC	ATT	ACT	CTG	CGA	CTG	GCC	CGG	TCC	ACC	CTG	CTG	CTC	ATC	CCA	1405				
Ser	Thr	Ile	Thr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu	Leu	Leu	Ile	Pro					
430					435					440										
CTA	TTC	GGA	ATC	CAC	TAC	ACA	GTA	TTT	GCC	TTC	TCC	CCA	GAG	AAT	GTC	1453				
Leu	Phe	Gly	Ile	His	Tyr	Thr	Val	Phe	Ala	Phe	Ser	Pro	Glu	Asn	Val					
445					450					455					460					
AGC	AAA	AGG	GAA	AGA	CTC	GTG	TTT	GAG	CTG	GGG	CTG	GGC	TCC	TTC	CAG	1501				
Ser	Lys	Arg	Glu	Arg	Leu	Val	Phe	Glu	Leu	Gly	Leu	Gly	Ser	Phe	Gln					
					465					470					475					
GGC	TTT	GTG	GTG	GCT	GTT	CTC	TAC	TGT	TTT	CTG	AAT	GGT	GAG	GTA	CAA	1549				
Gly	Phe	Val	Val	Ala	Val	Leu	Tyr	Cys	Phe	Leu	Asn	Gly	Glu	Val	Gln					
					480					485					490					
GCG	GAG	ATC	AAG	CGA	AAA	TGG	CGA	AGC	TGG	AAG	GTG	AAC	CGT	TAC	TTC	1597				
Ala	Glu	Ile	Lys	Arg	Lys	Trp	Arg	Ser	Trp	Lys	Val	Asn	Arg	Tyr	Phe					
					495					500					505					
GCT	GTG	GAC	TTC	AAG	CAC	CGA	CAC	CCG	TCT	CTG	GCC	AGC	AGT	GGG	GTG	1645				
Ala	Val	Asp	Phe	Lys	His	Arg	His	Pro	Ser	Leu	Ala	Ser	Ser	Gly	Val					
					510					515					520					
AAT	GGG	GGC	ACC	CAG	CTC	TCC	ATC	CTG	AGC	AAG	AGC	AGC	TCC	CAA	ATC	1693				
Asn	Gly	Gly	Thr	Gln	Leu	Ser	Ile	Leu	Ser	Lys	Ser	Ser	Ser	Gln	Ile					
525					530					535					540					
CGC	ATG	TCT	GGC	CTC	CCT	GCT	GAC	AAT	CTG	GCC	ACC	TGAGCC	ATGC	TCCCCT		1745				
Arg	Met	Ser	Gly	Leu	Pro	Ala	Asp	Asn	Leu	Ala	Thr									
					545					550										

FIG. 17C

AGCCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGCTG	60
GCCAAGAAGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT GCT CAC	109
Met Ala Gly Val Val His Val Ser Leu Ala Ala His	
1 5 10	
TGC GGG GCC TGT CCG TGG GGC CGG GGC AGA CTC CGC AAA GGA CGC GCA	157
Cys Gly Ala Cys Pro Trp Gly Arg Gly Arg Leu Arg Lys Gly Arg Ala	
15 20 25	
GCC TGC AAG TCC GCG GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG	205
Ala Cys Lys Ser Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu	
30 35 40	
CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA AGT GTC ATG GCT GGT	253
Leu Ser Val Gly Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly	
45 50 55 60	
GTC GTG CAC GTT TCC CTG GCT GCT CTC CTC CTG CTG CCT ATG GCC CCT	301
Val Val His Val Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Pro	
65 70 75	
GCC ATG CAT TCT GAC TGC ATC TTC AAG AAG GAG CAA GCC ATG TGC CTG	349
Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu	
80 85 90	
GAG AAG ATC CAG AGG GCC AAT GAG CTG ATG GGC TTC AAT GAT TCC TCT	397
Glu Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser	
95 100 105	
CCA GGC TGT CCT GGG ATG TGG GAC AAC ATC ACG TGT TGG AAG CCC GCC	445
Pro Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala	
110 115 120	
CAT GTG GGT GAG ATG GTC CTG GTC AGC TGC CCT GAG CTC TTC CGA ATC	493
His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile	
125 130 135 140	
TTC AAC CCA GAC CAA GTC TGG GAG ACC GAA ACC ATT GGA GAG TCT GAT	541
Phe Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp	
145 150 155	
TTT GGT GAC AGT AAC TCC TTA GAT CTC TCA GAC ATG GGA GTG GTG AGC	589
Phe Gly Asp Ser Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser	
160 165 170	
CGG AAC TGC ACG GAG GAT GGC TGG TCG GAA CCC TTC CCT CAT TAC TTT	637
Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe	
175 180 185	
GAT GCC TGT GGG TTT GAT GAA TAT GAA TCT GAG ACT GGG GAC CAG GAT	685
Asp Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp	

FIG. 18A

190	195	200	
TAT Tyr 205	TAC Tyr	TAC Tyr	CTG Leu
TCA Ser	GTG Val 210	AAG Lys	GCC Ala
CTC Leu	TAC Tyr	ACG Thr 215	GTT Val
GGC Tyr	TAC Ser	AGC Thr 220	ACA Thr
733			
TCC Ser	CTC Leu	GTC Val	ACC Thr 225
CTC Leu	ACC Thr 225	ACT Thr	GCC Ala
ATG Met	GTC Val 230	ATC Ile	CTT Leu
TGT Cys	CGC Arg	TTC Phe 235	CGG Arg
781			
AAG Lys	CTG Leu	CAC His	TGC Cys 240
ACA Thr	CGC Arg	AAC Asn	TTC Phe 245
ATC Ile 245	CAC His	ATG Met	AAC Asn 250
CTG Leu	TTT Phe 250	GTG Val	TCG Ser
829			
TTC Phe	ATG Met	CTG Leu 255	AGG Arg
GCG Ala	ATC Ile	TCC Ser	GTC Val 260
TTC Phe	ATC Ile	AAA Lys	GAC Asp 265
TGG Trp 265	ATT Ile	CTG Leu	TAT Tyr
877			
GCG Ala	GAG Glu 270	CAG Gln	GAC Asp
AGC Ser	AAC Asn	CAC His 275	TGC Cys
TTC Phe	ATC Ile	TCC Ser	ACT Thr 280
GTG Val	GAA Glu	TGT Cys	AAG Lys
925			
GCC Ala 285	GTC Val	ATG Met	GTT Val
TTC Phe 290	TTC Phe 290	CAC His	TAC Tyr
TGT Cys	GTT Val	GTG Val 295	TCC Ser
AAC Asn	TAC Tyr	TTC Phe	TGG Trp 300
973			
CTG Leu	TTC Phe	ATC Ile	GAG Glu 305
GGC Gly 305	CTG Leu	TAC Tyr	CTC Leu
TTC Phe	ACT Thr 310	CTG Leu	CTG Leu
GTG Val	GAG Glu 315	ACC Thr 315	TTC Phe
1021			
TTC Phe	CCT Pro	GAA Glu	AGG Arg 320
AGA Arg	TAC Tyr	TTC Phe	TAC Tyr
TGG Trp 325	TAC Tyr	ACC Thr	ATC Ile
ATT Ile	GGC Gly 330	TGG Trp	GGG Gly
1069			
ACC Thr	CCA Pro	ACT Thr 335	GTG Val
TGT Cys	GTG Val	ACA Thr 340	GTG Val
TGG Trp	GCT Ala	ACG Thr	CTG Leu
AGA Arg 345	CTC Leu	TAC Tyr	TTT Phe
1117			
GAT Asp	GAC Asp 350	ACA Thr	GGC Gly
TGC Cys	TGG Trp	GAT Asp 355	ATG Met
AAT Asn	GAC Asp	AGC Ser	ACA Thr 360
GCT Ala	CTG Leu	TGG Trp	TGG Trp
1165			
GTG Val 365	ATC Ile	AAA Lys	GGC Gly
CCT Pro	GTG Val 370	GTT Val	GGC Gly
TCT Ser	ATC Ile	ATG Met 375	GTT Val
AAC Asn	TTT Phe	GTG Val 380	CTT Leu
1213			
TTT Phe	ATT Ile	GGC Gly	ATT Ile
ATC Ile 385	GTC Val	ATC Ile	CTT Leu
GTG Val	CAG Gln 390	AAA Lys	CTT Leu
CAG Gln	TCT Ser	CCA Pro 395	GAC Asp
1261			
ATG Met	GGA Gly	GGC Gly	AAT Asn 400
GAG Glu	TCC Ser	AGC Ser	ATC Ile
TAC Tyr 405	TTA Leu	ACA Thr	AAT Asn
TTA Leu	AGC Ser 410	CCG Pro	CGA Arg
1309			

FIG. 18B

GTC CCC AAG AAA GCC CGA GAG GAC CCC CTG CCT GTG CCC TCA GAC CAG	1357
Val Pro Lys Lys Ala Arg Glu Asp Pro Leu Pro Val Pro Ser Asp Gln	
415 420 425	
CAT TCA CTC CCT TTC CTG CGA CTG GCC CGG TCC ACC CTG CTG CTC ATC	1405
His Ser Leu Pro Phe Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile	
430 435 440	
CCA CTA TTC GGA ATC CAC TAC ACA GTA TTT GCC TTC TCC CCA GAG AAT	1453
Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn	
445 450 455 460	
GTC AGC AAA AGG GAA AGA CTC GTG TTT GAG CTG GGG CTG GGC TCC TTC	1501
Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe	
465 470 475	
CAG GGC TTT GTG GTG GCT GTT CTC TAC TGT TTT CTG AAT GGT GAG GTA	1549
Gln Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val	
480 485 490	
CAA GCG GAG ATC AAG CGA AAA TGG CGA AGC TGG AAG GTG AAC CGT TAC	1597
Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr	
495 500 505	
TTC GCT GTG GAC TTC AAG CAC CGA CAC CCG TCT CTG GCC AGC AGT GGG	1645
Phe Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly	
510 515 520	
GTG AAT GGG GGC ACC CAG CTC TCC ATC CTG AGC AAG AGC AGC TCC CAA	1693
Val Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln	
525 530 535 540	
ATC CGC ATG TCT GGC CTC CCT GCT GAC AAT CTG GCC ACC TGAGCCATGC TCC	1745
Ile Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr ***	
545 550	
CCT	1748

FIG. 18C

may vary with time in the case of the present invention.

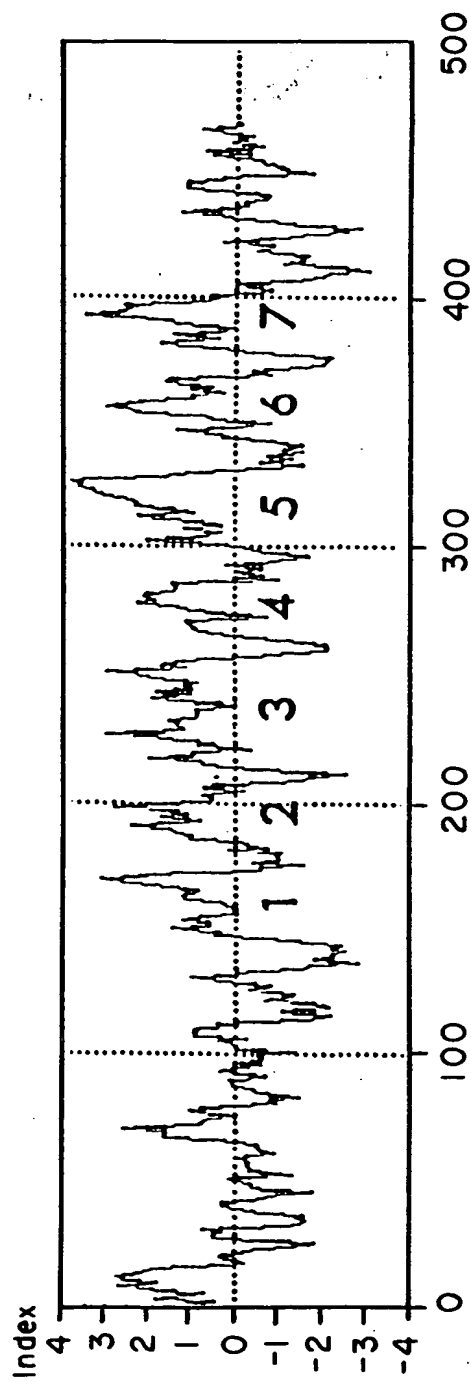


FIG. 19A

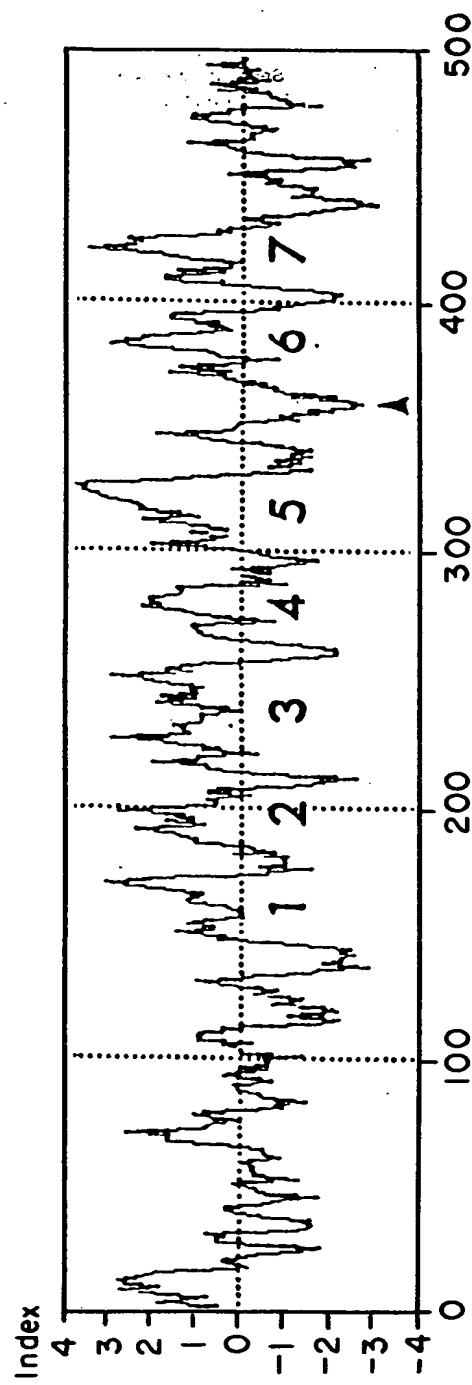


FIG. 19B



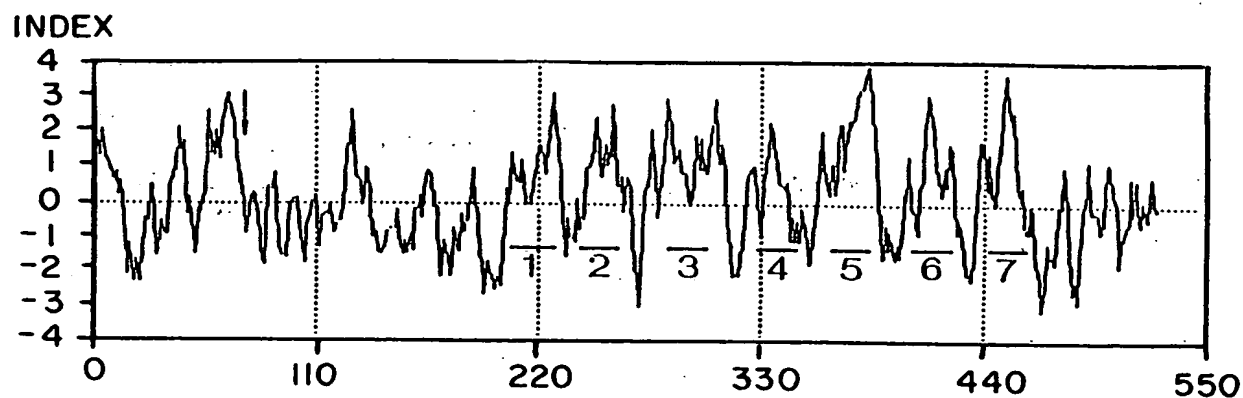


FIG. 21

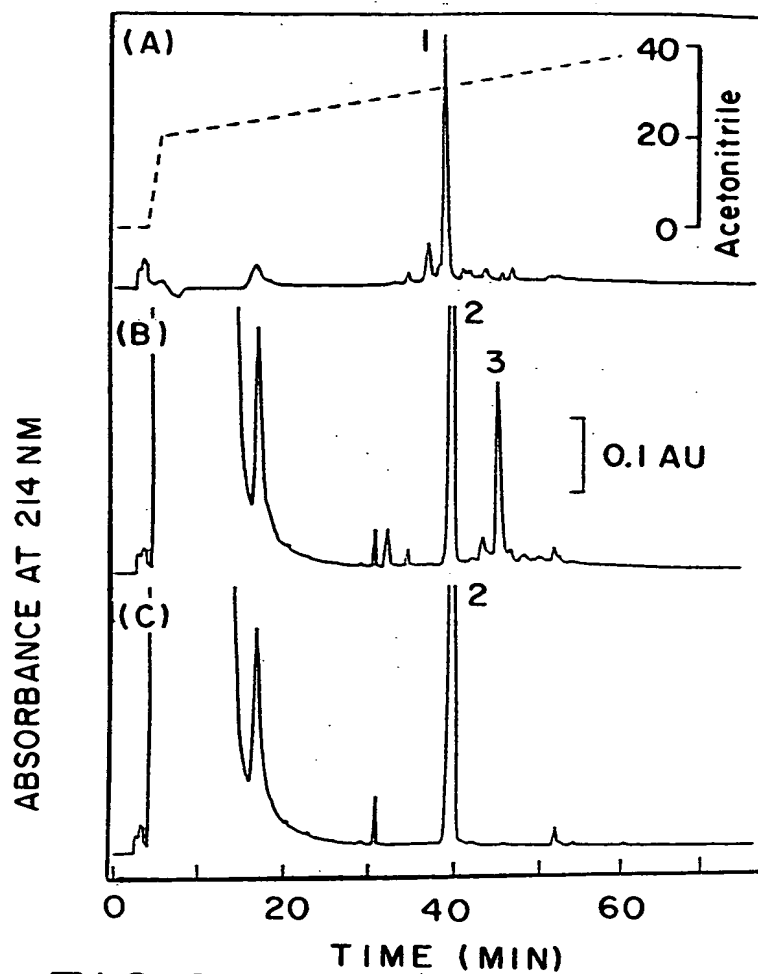


FIG. 28

[illegible]

August 19, 1900



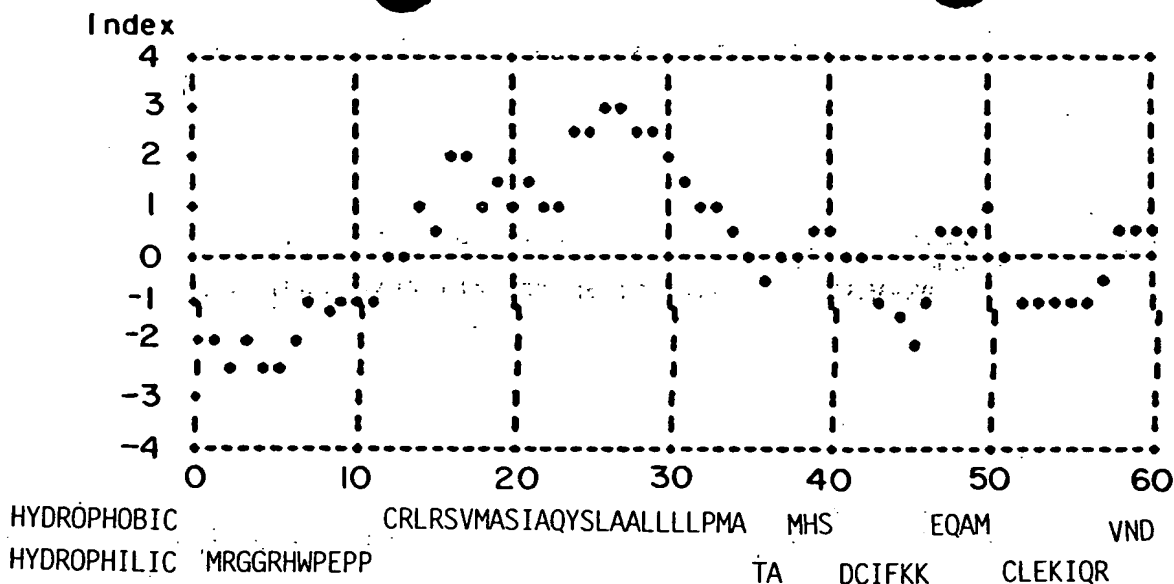


FIG.23A

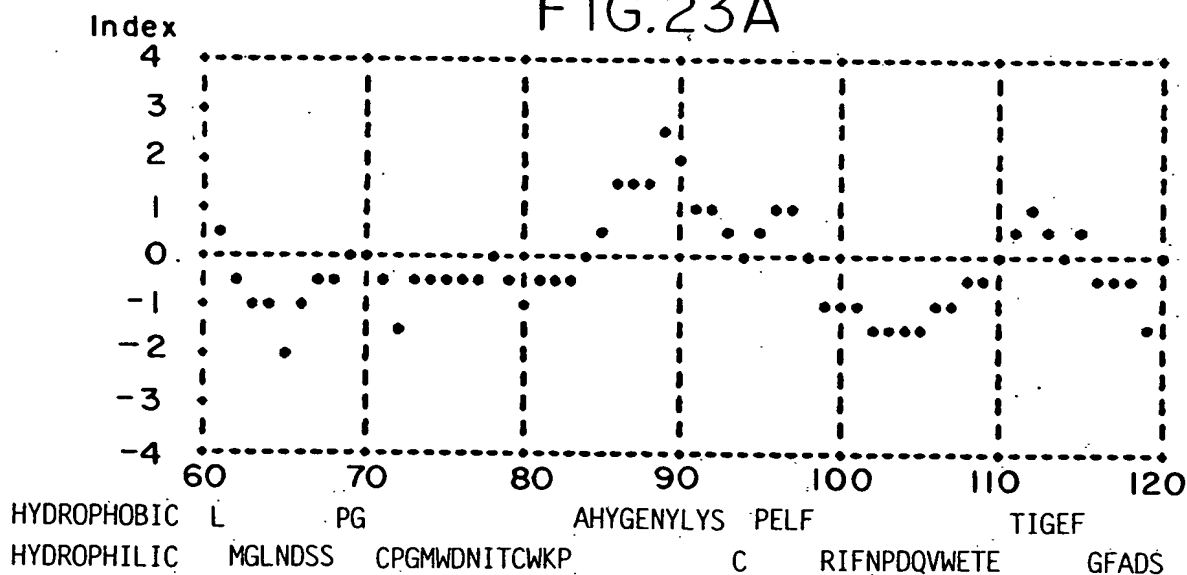


FIG.23B

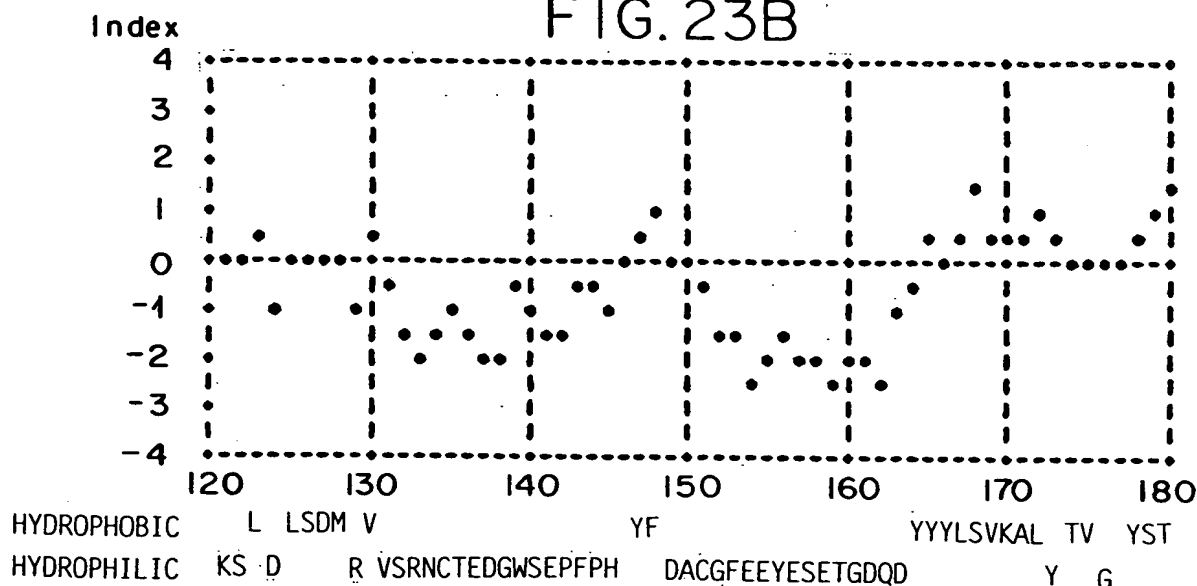


FIG.23C

COPY OF  
ORIGINAL

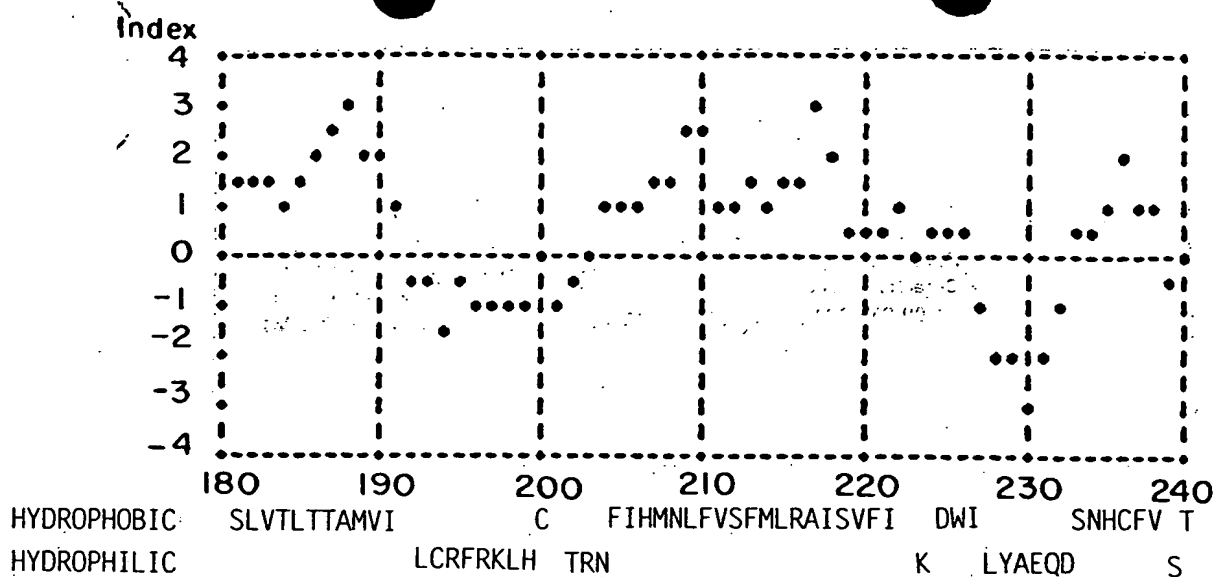


FIG.23D

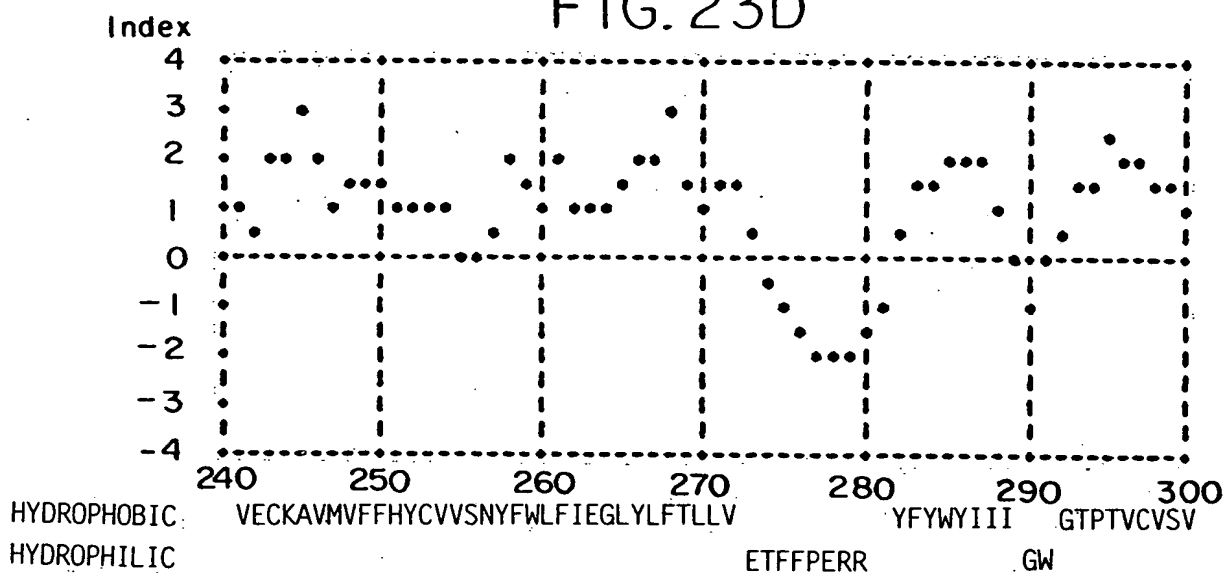


FIG.23E

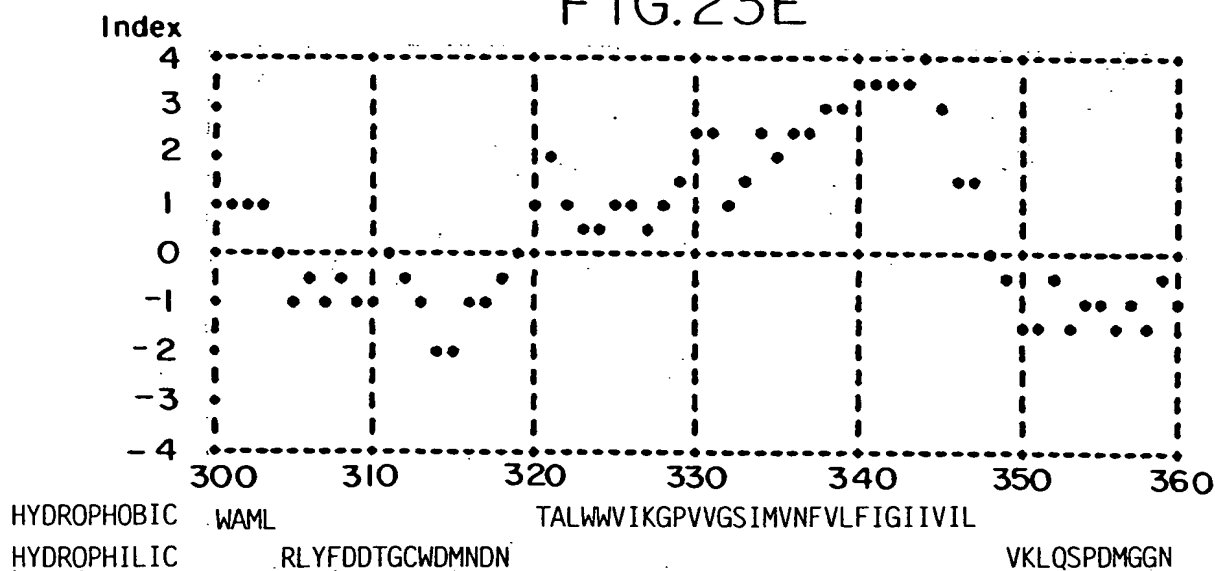


FIG.23F

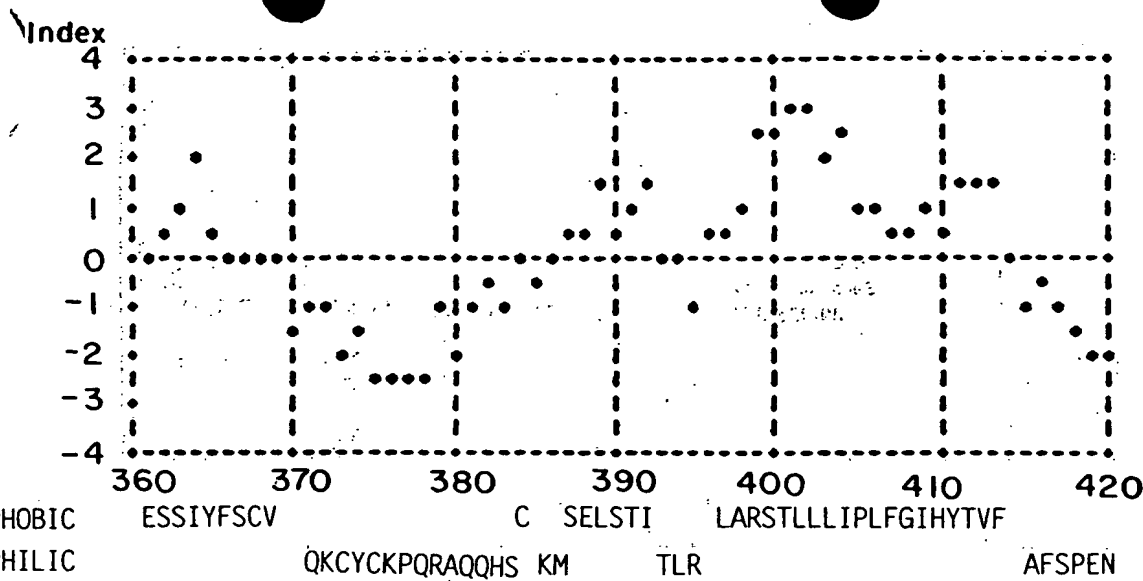


FIG.23G

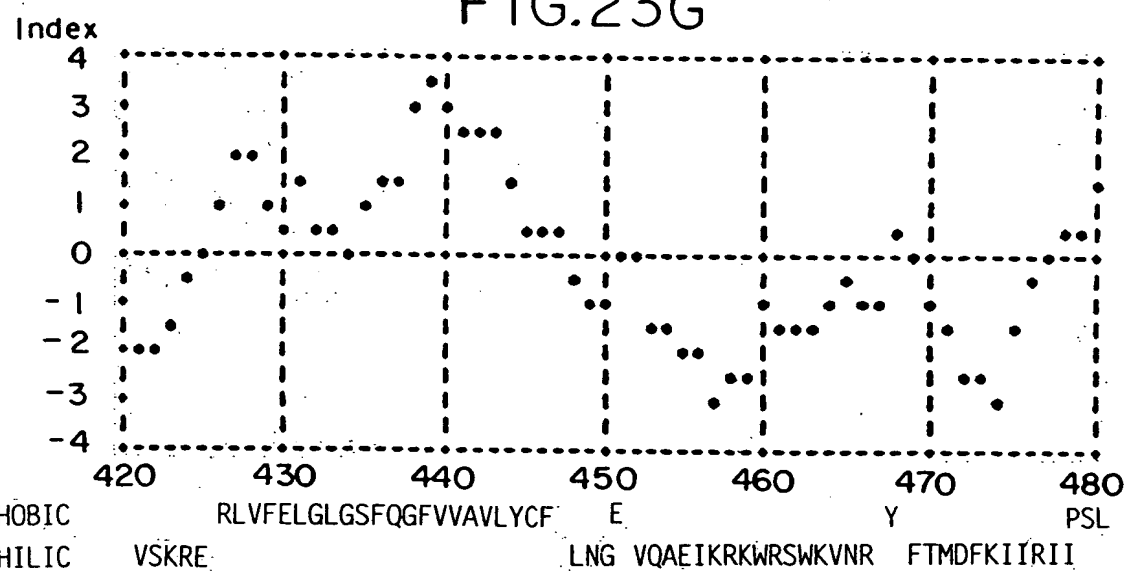


FIG.23H

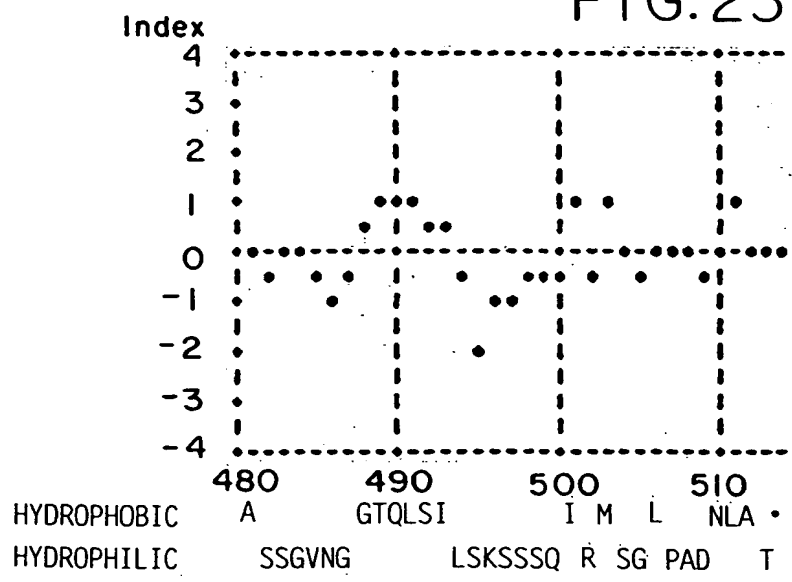


FIG.23I

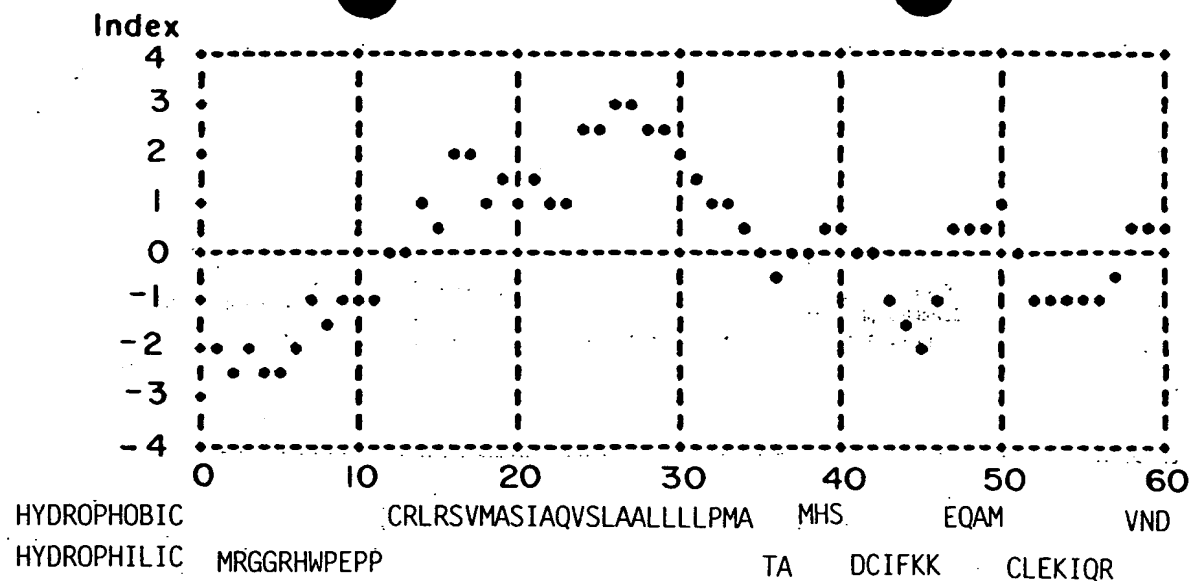


FIG. 24A

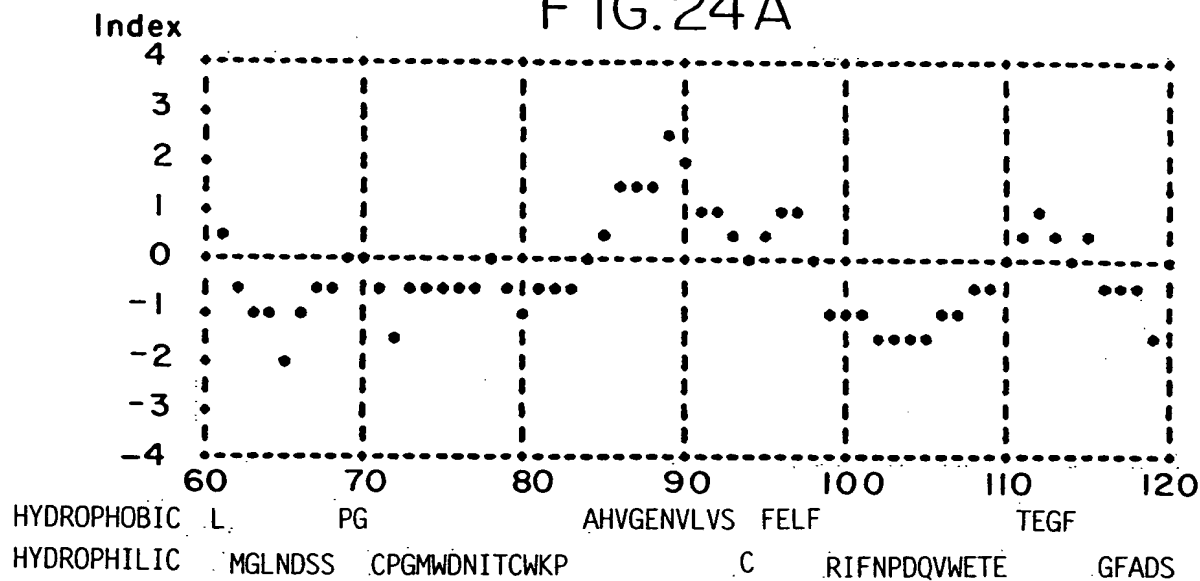


FIG. 24B

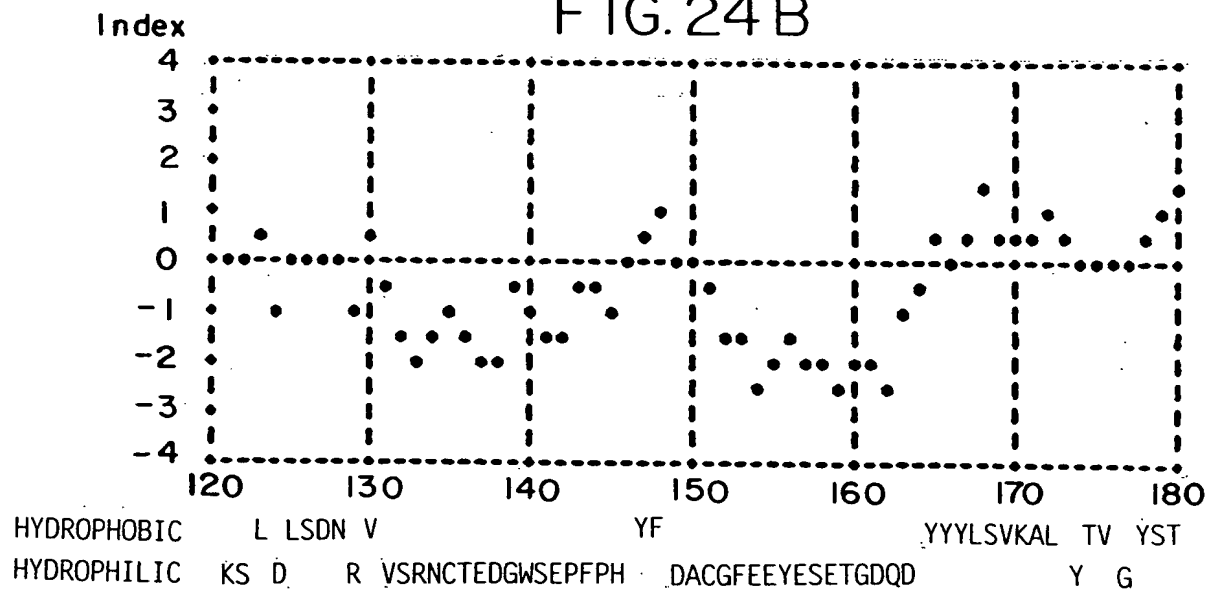


FIG. 24C

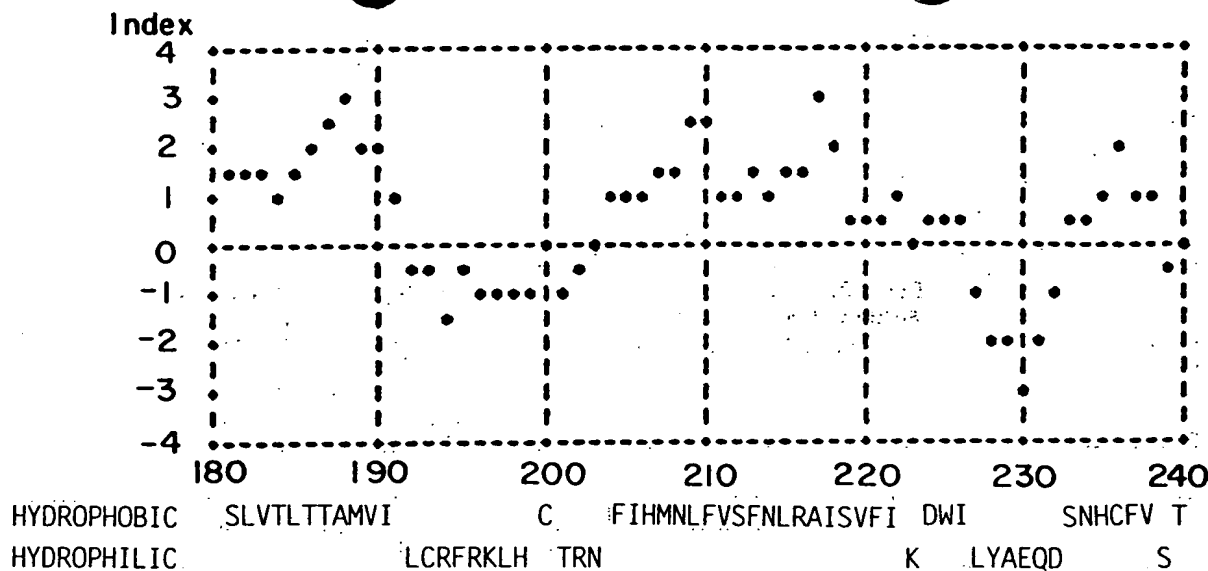


FIG. 24D

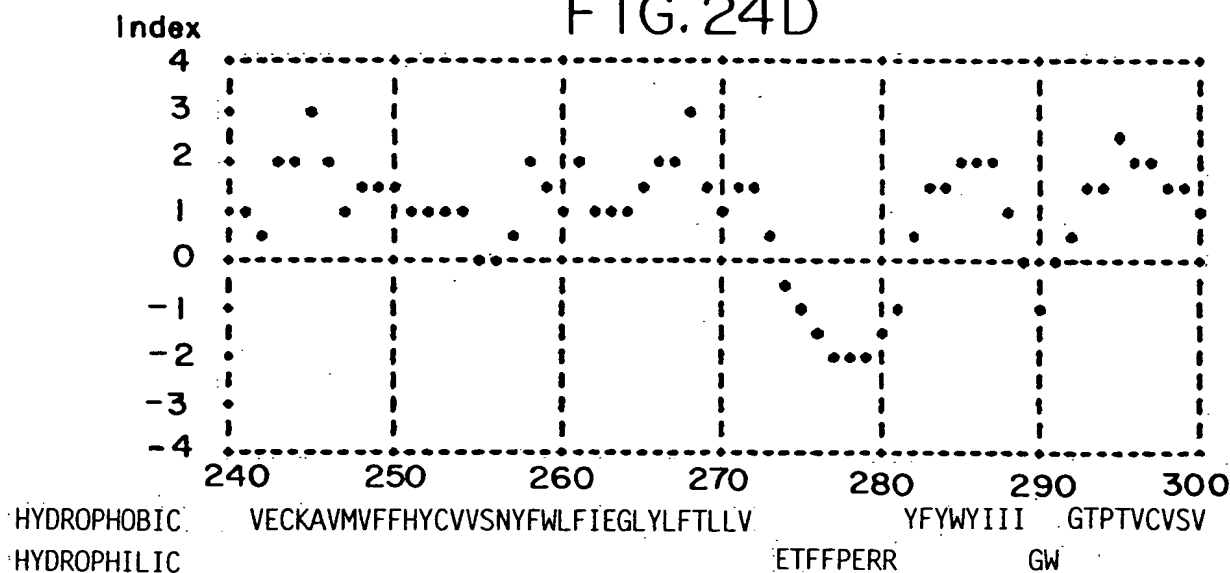


FIG. 24E

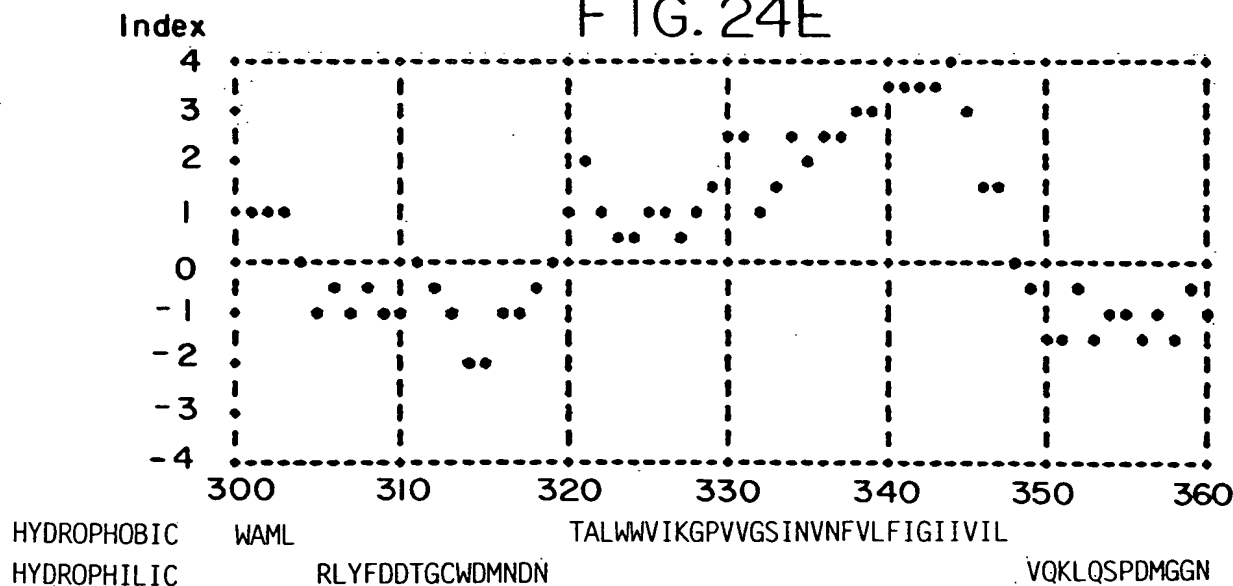


FIG. 24F

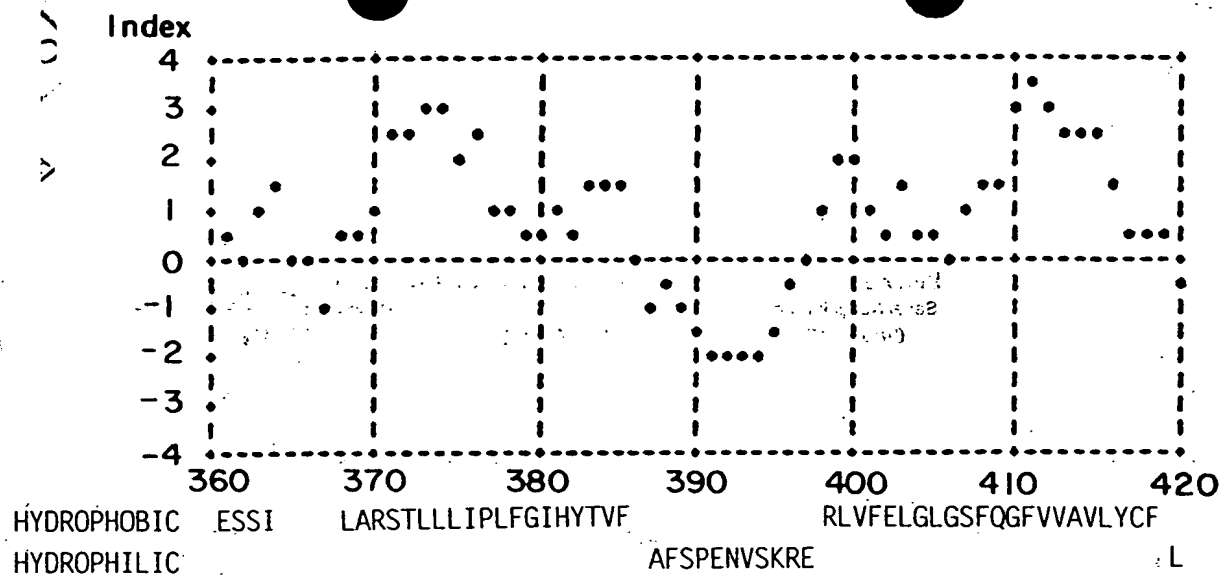


FIG. 24G

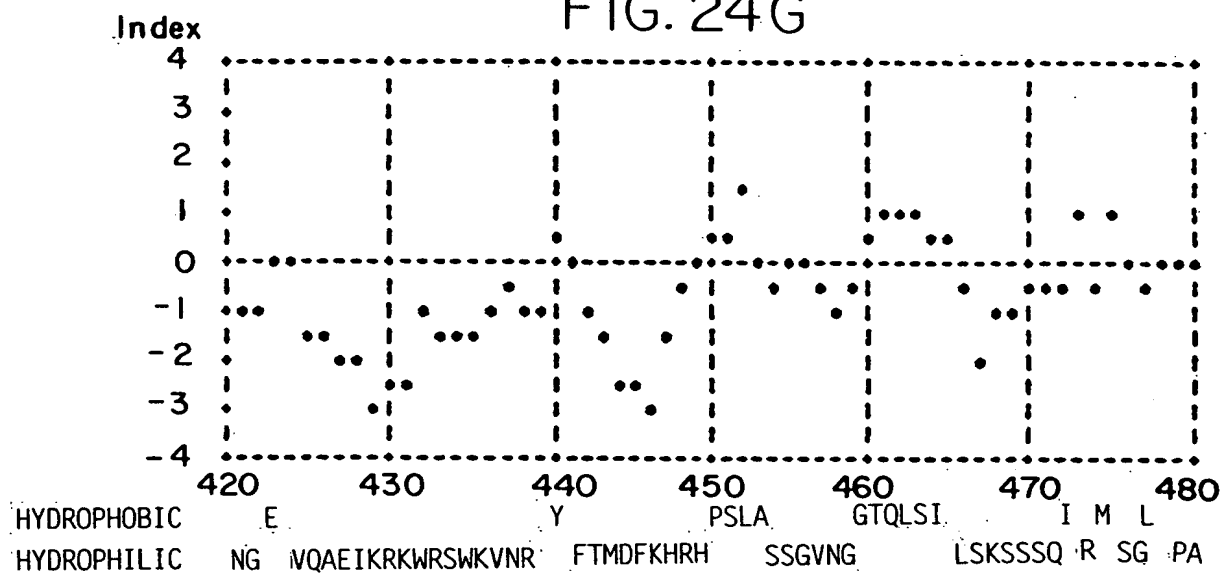


FIG. 24H

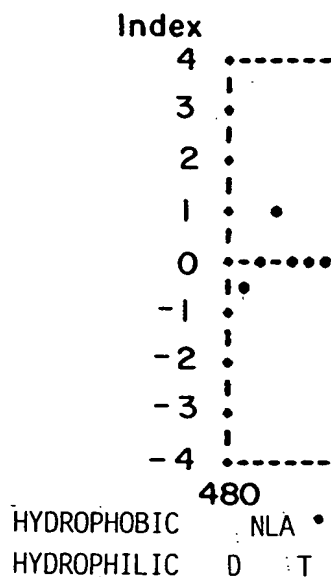
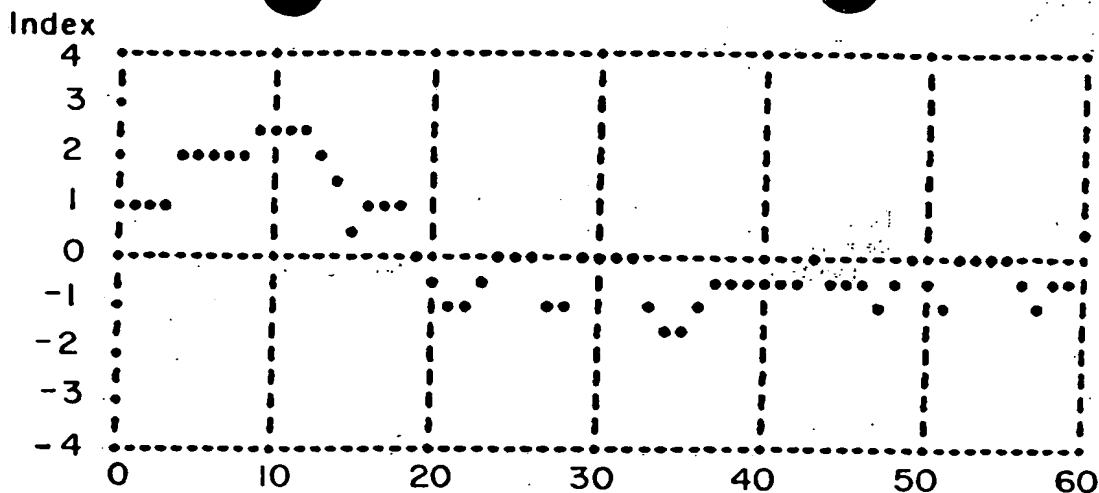


FIG. 24I

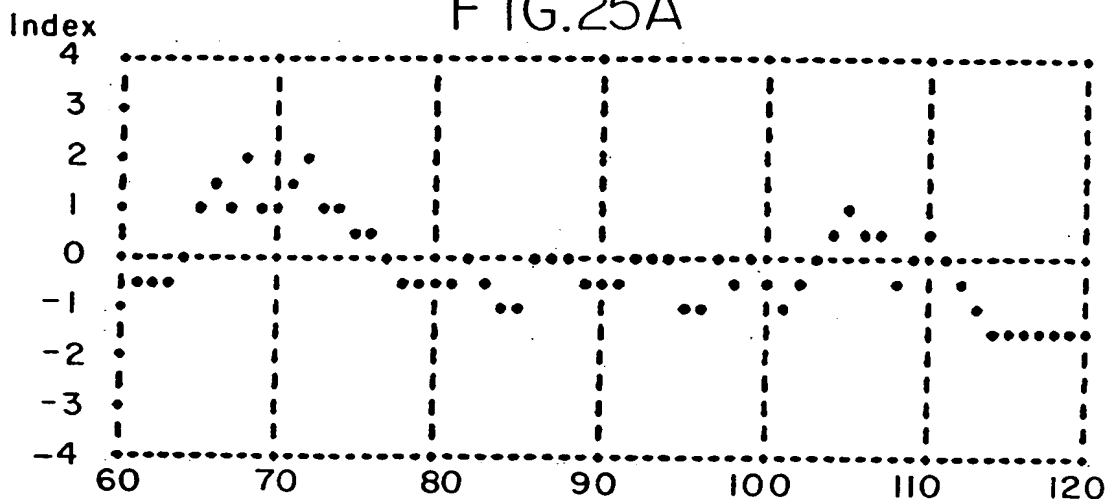


HYDROPHOBIC MARVLQLSLTALLLPVAIA

HYDROPHILIC :MHSDCIFKKEQANCLERIQRANDLMGLNESSPGCPMWDN

I

FIG.25A



HYDROPHOBIC PAQVGENVLVSC

HYDROPHILIC TCWK

I

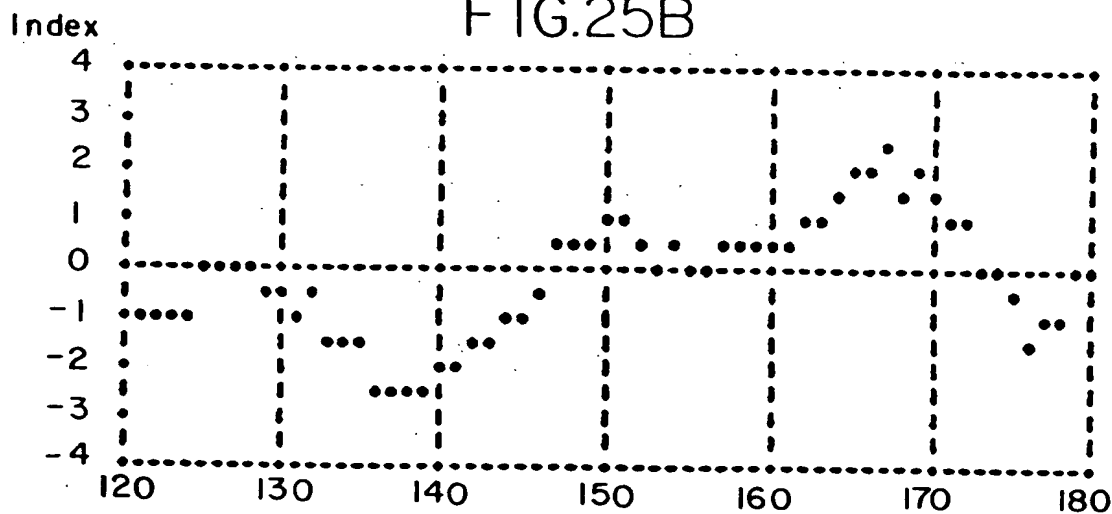
QV

F

SLEI DN

FEVER FNPD WMTETIGDSG ADSN T GVVGRNCTED

FIG.25B



HYDROPHOBIC

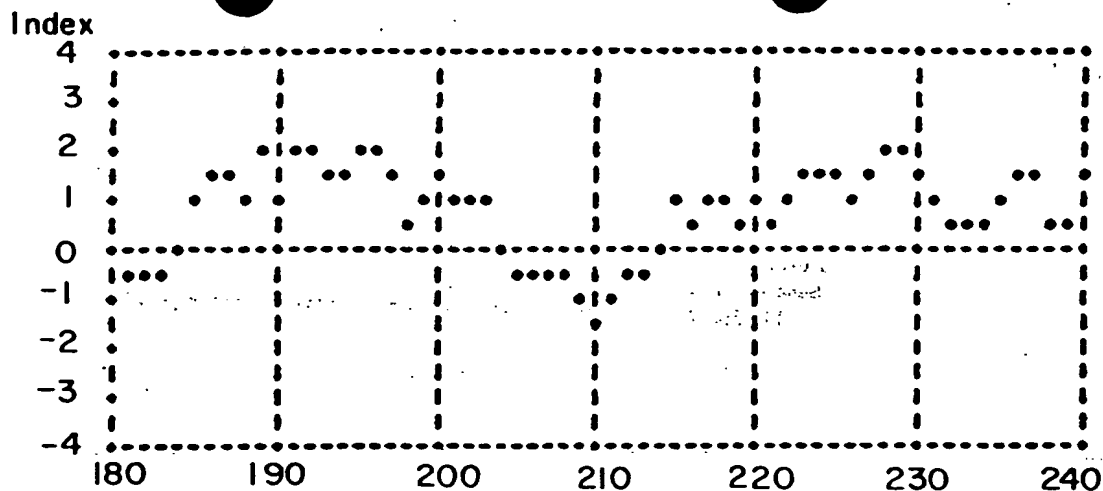
HYDROPHILIC

GWSEPFPHYFDACGFDDYEPESGDQD

YYLSVKALYTVGYSTSLATLTANVI

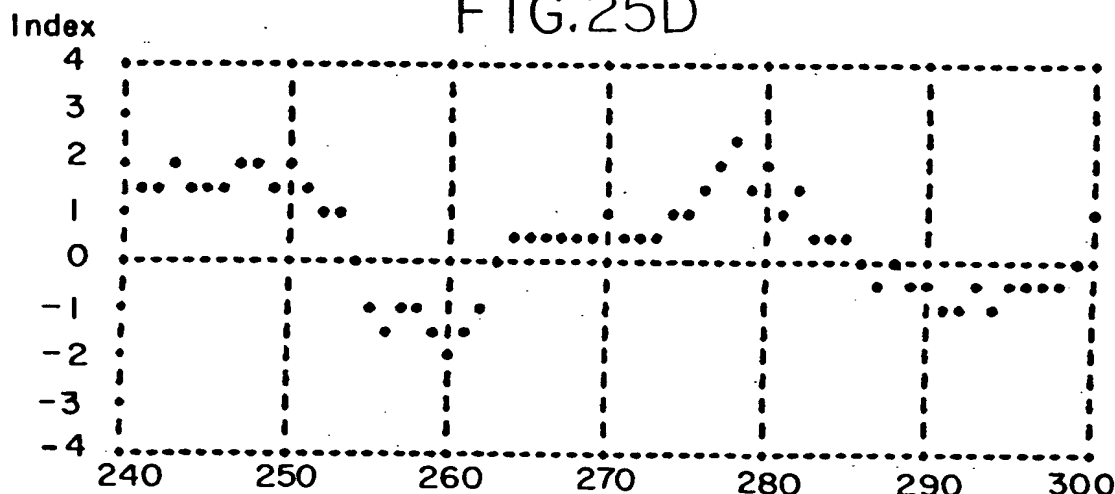
LCRFRKL

FIG.25C



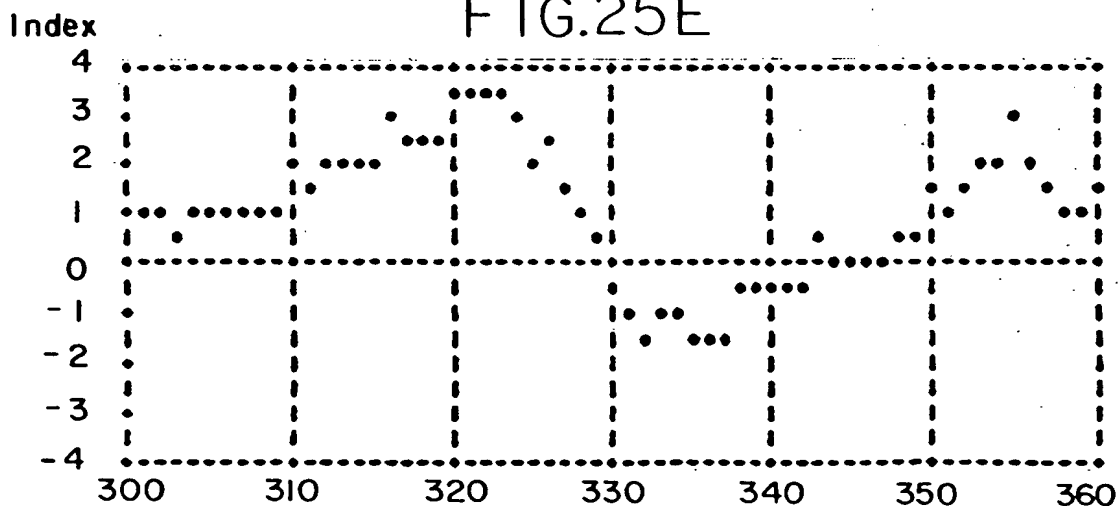
HYDROPHOBIC RNF IHMNL FVS FMLRAISVFI SSHCFVSTVECKAVMVFFHYCVVSNY  
HYDROPHILIC HCT KDWILYAEQD

FIG. 25D



HYDROPHOBIC FWLFIEGLYLFTL RYFYWYTIIGWGTPTVCVTWAV L D  
HYDROPHILIC LVETFFPER LR YFDDAGCWDMMN

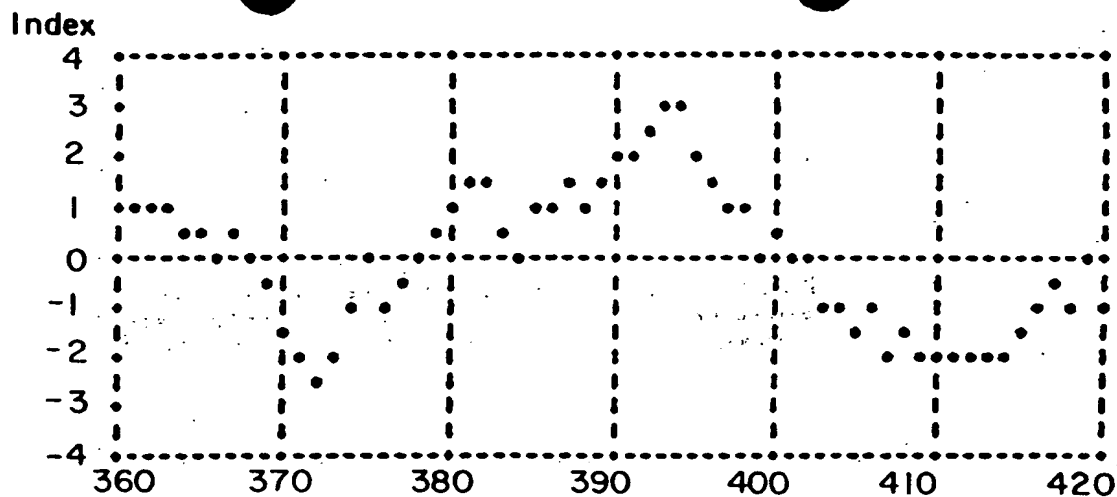
FIG. 25E



HYDROPHOBIC STALWWVIKGPVVGSI MVMVLF IGI III KSSIYLR LARSTLLL IPL  
HYDROPHILIC LVQKLQSPDMGGN

FIG. 25F





HYDROPHOBIC

FGIHTYVF

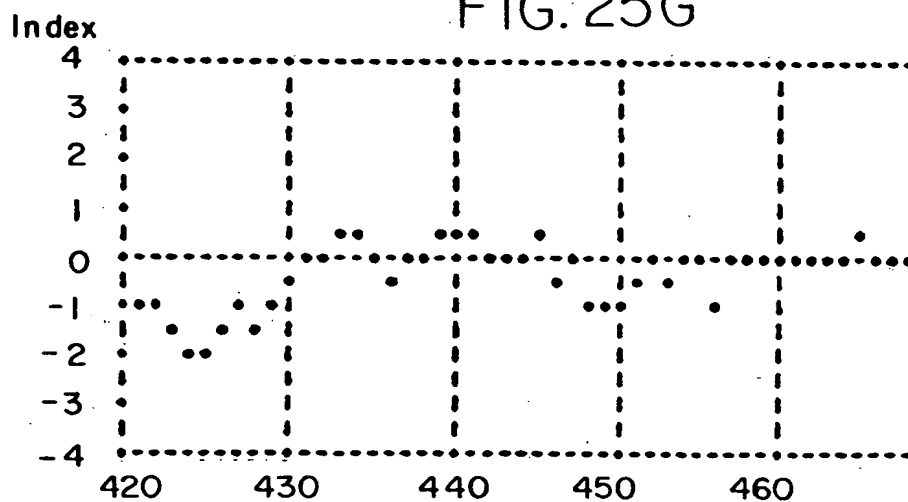
ERLVEFELGLGSFQGFVAVLYC

HYDROPHILIC

AFSPENVSKR

FLNGEVQAEIKKKWRSWKVN

FIG. 25G



HYDROPHOBIC

HPSL

VNGGTQL I

QL MSSL

NLA •

HYDROPHILIC

RYFTMDFKHR

ASSG

S LSKSS

R

PAD

T

FIG. 25H

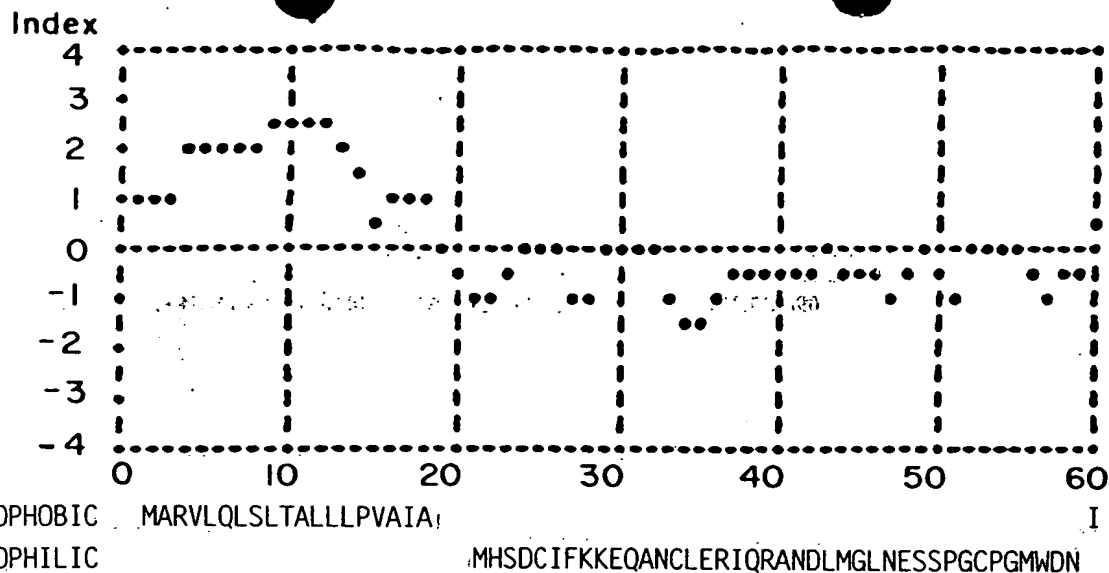


FIG. 26A

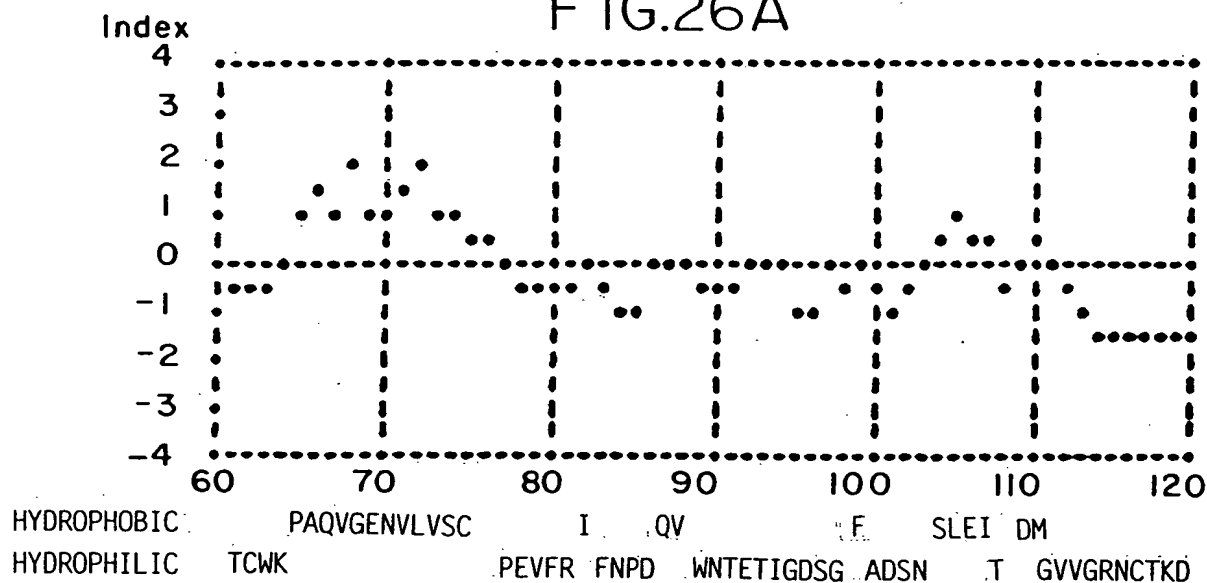


FIG. 26B

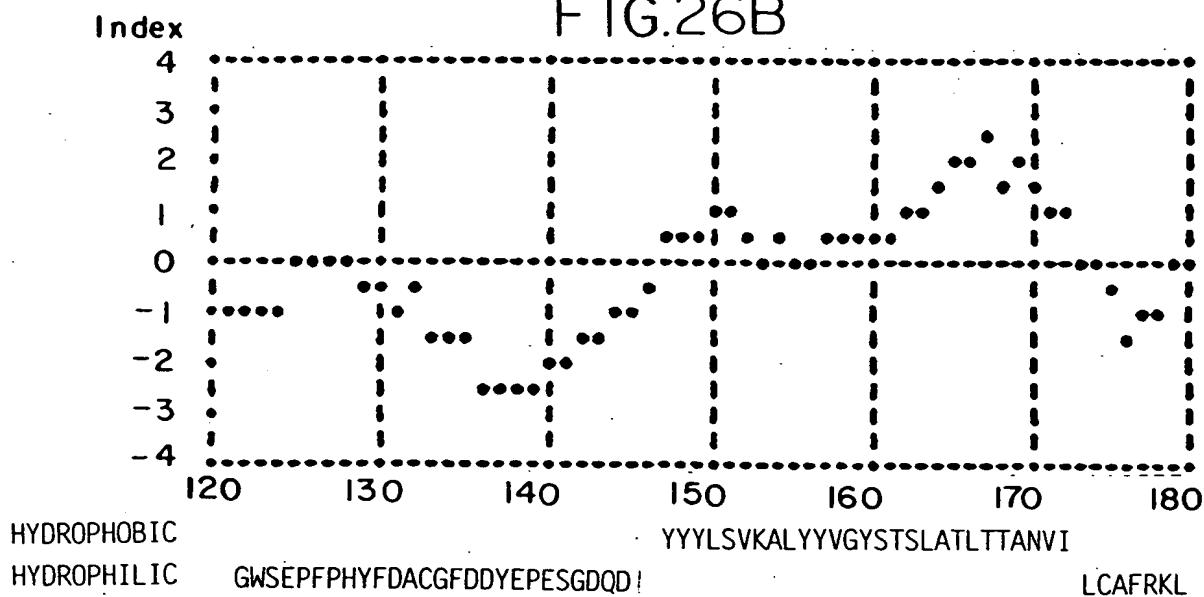


FIG. 26C

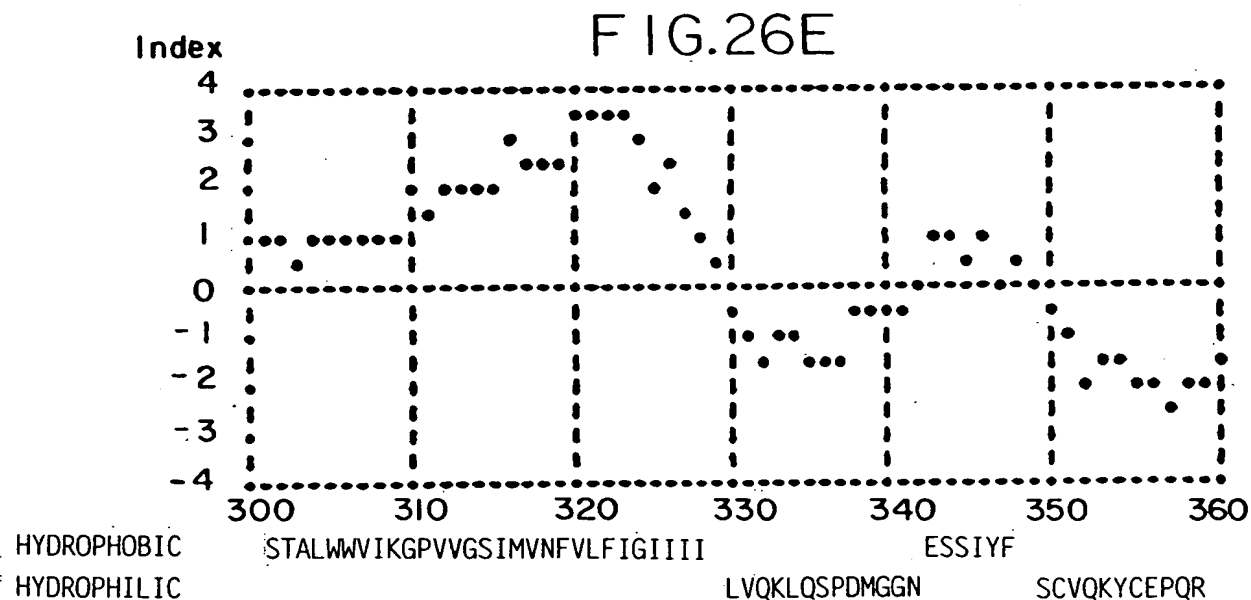
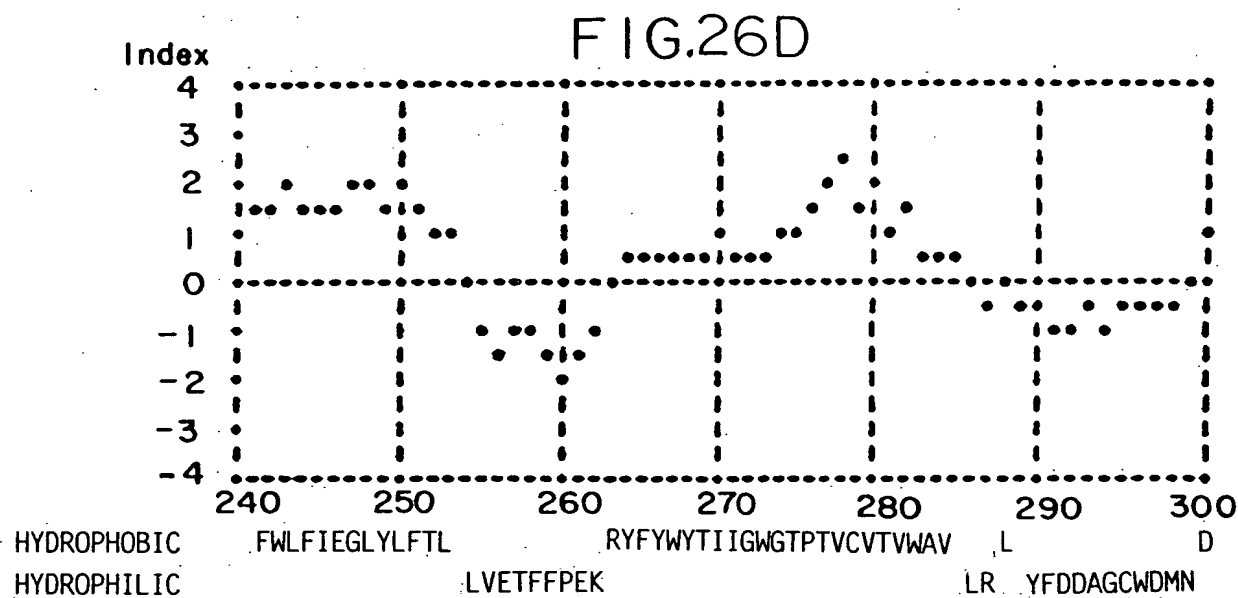
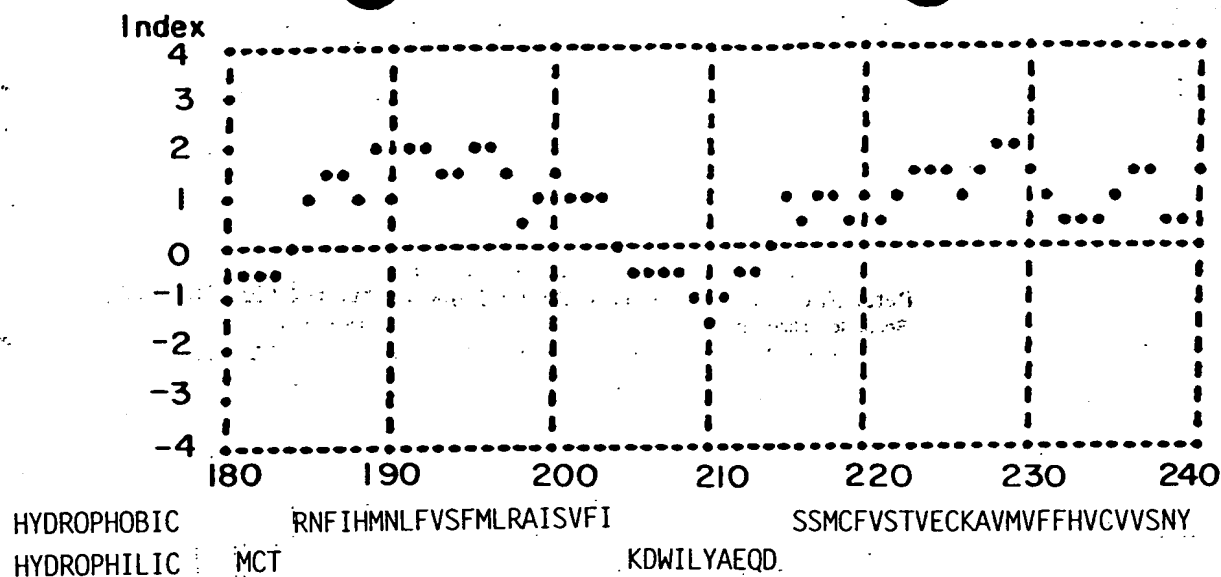
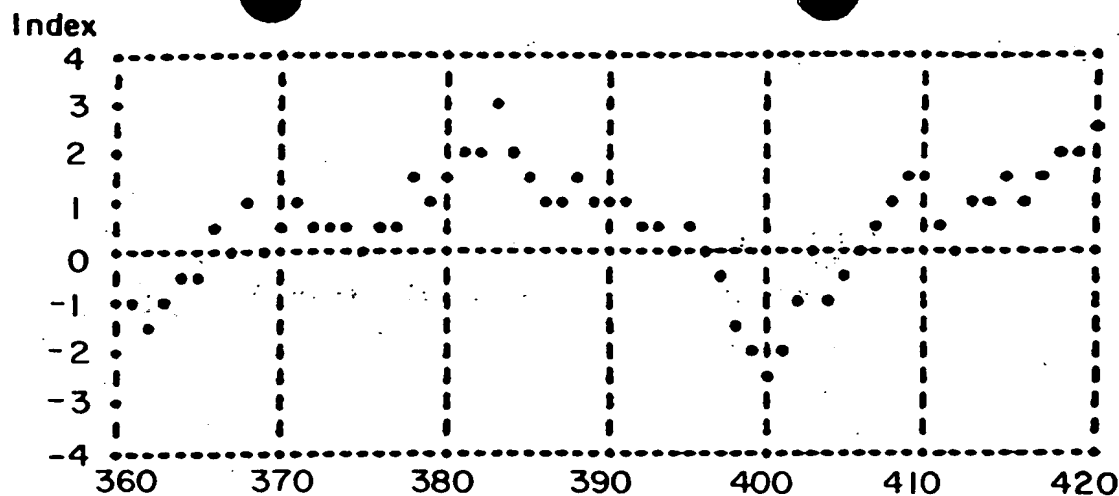
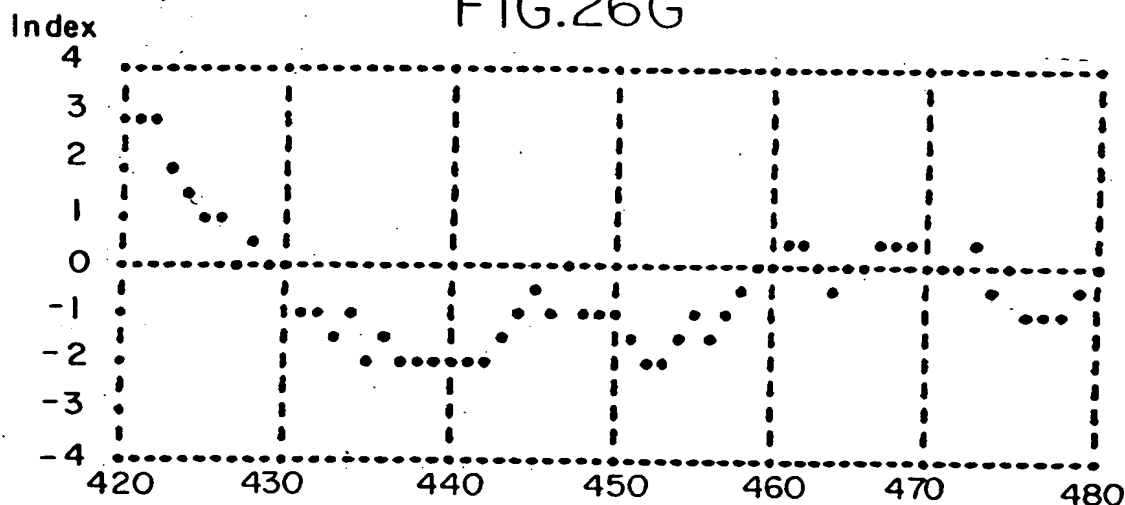


FIG.26F



HYDROPHOBIC C MSELSTITLRLARSTILLIPLFGIMYTVF ERLVFELGLGSFQG  
 HYDROPHILIC AQQHS K AFSPENVSKR

FIG.26G



HYDROPHOBIC FWAVLYC MPSL VMGGTQL I  
 HYDROPHILIC FLNGEVQAEIKRKWRSWKVNRYFTNDFEMR ASSG S LSRSS

FIG.26H

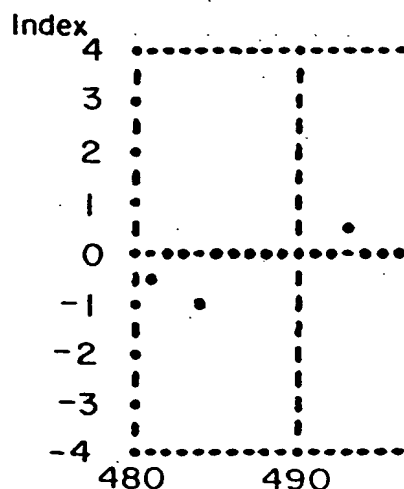


FIG.26I

HYDROPHOBIC QL MSSL NLA •  
 HYDROPHILIC S R PAD T

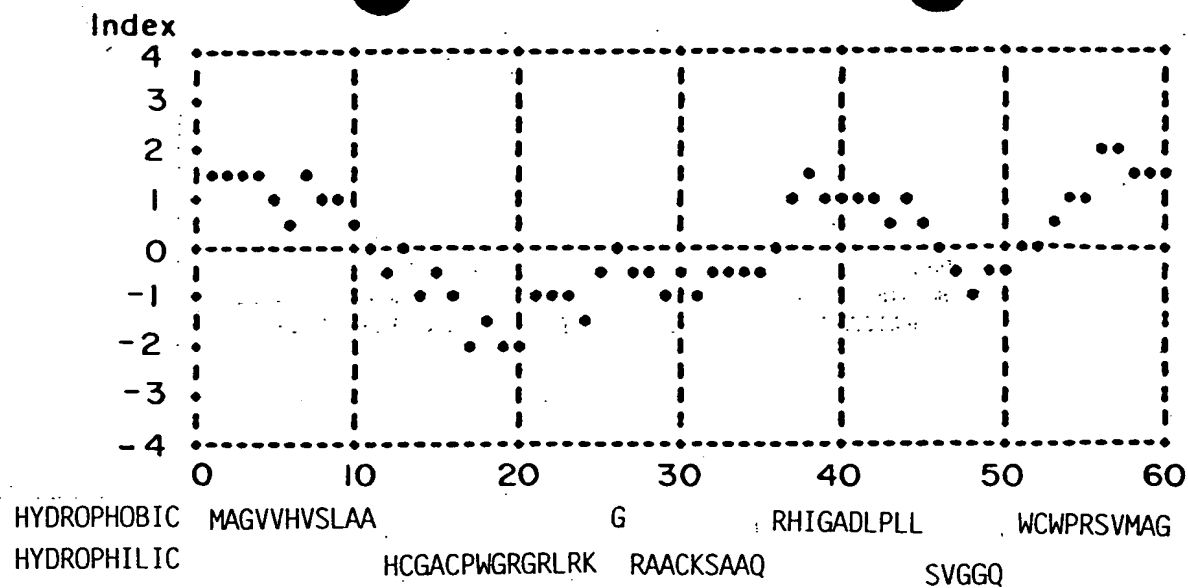


FIG.27A

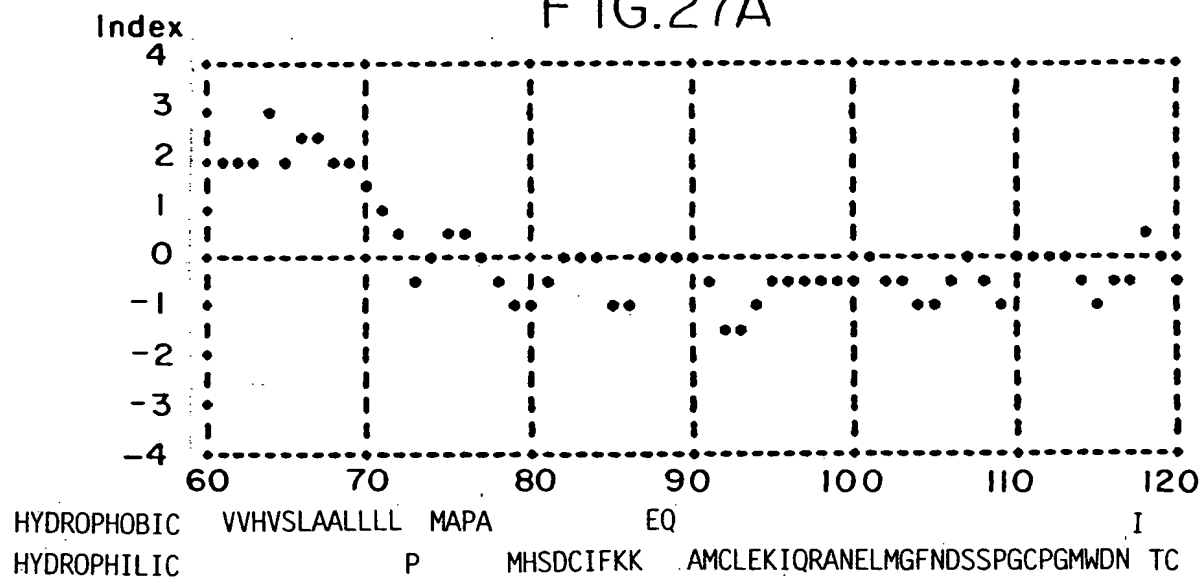


FIG.27B

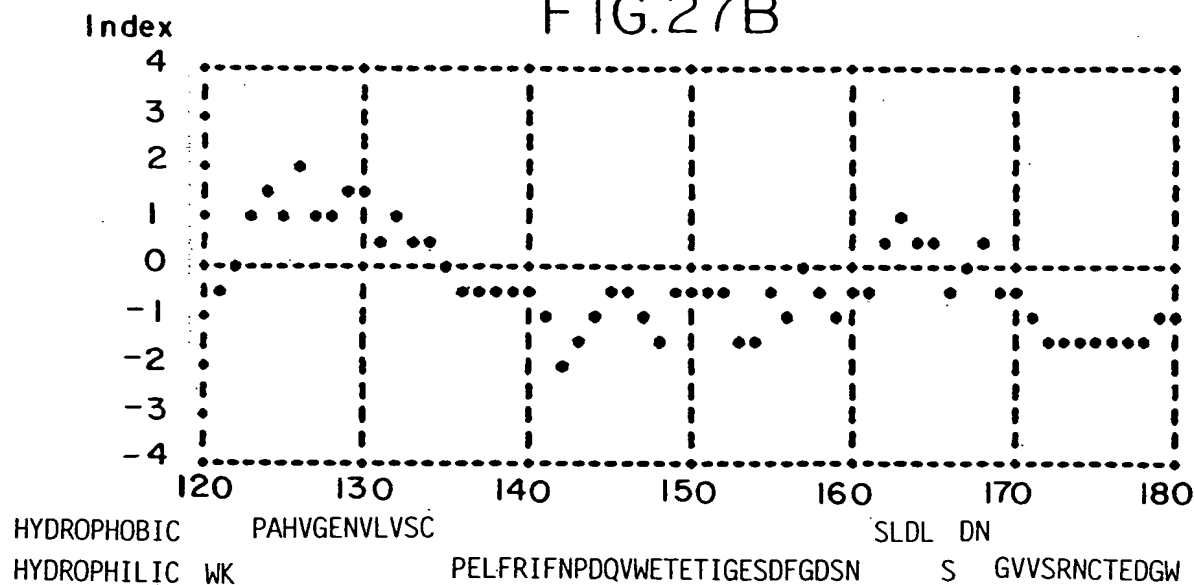
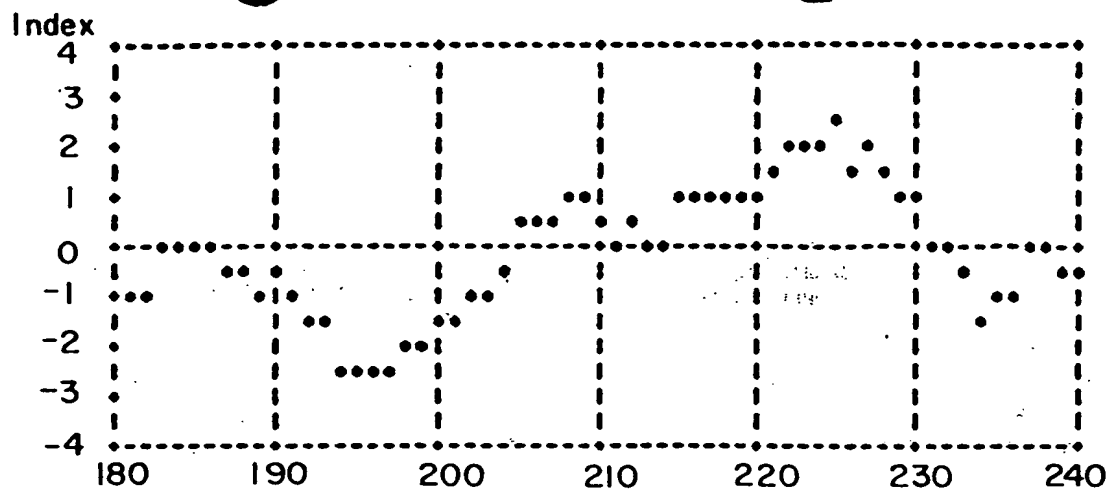


FIG.27C



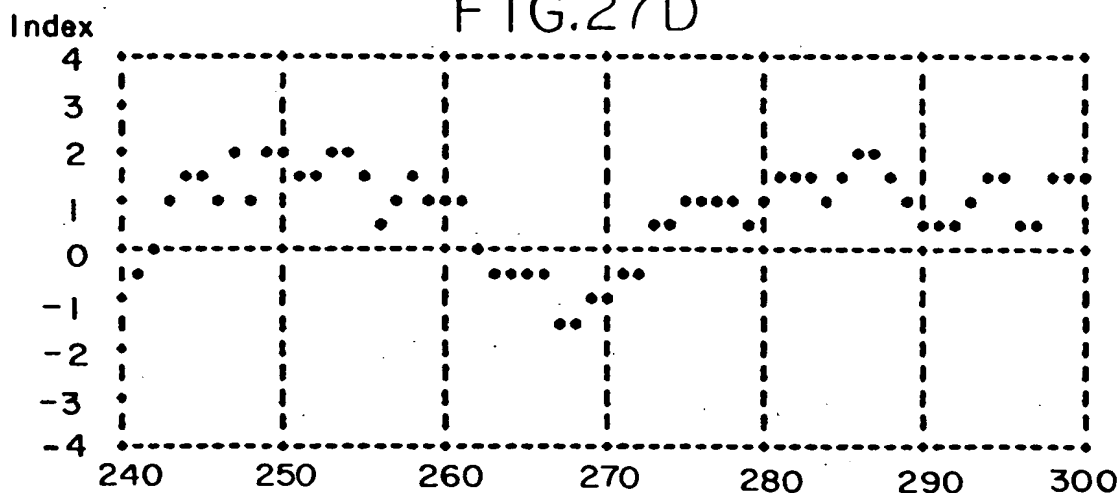
HYDROPHOBIC

YYLSVKALYTVGYSTSLVTLTTAMVI

HYDROPHILIC SEPFFHYFDACGFDEYESETGDQD

LCRFRKLHC

FIG.27D



HYDROPHOBIC

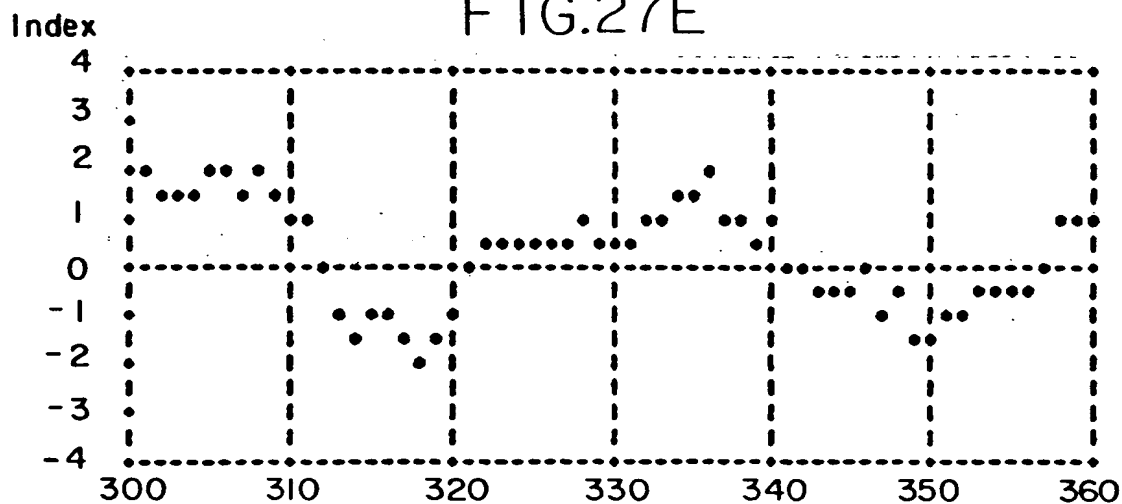
RNFIHMNLFVSFMLRAISVFI

SNHCFISTVECKAVMVFFHYCVVSNYFW

HYDROPHILIC T

KDWILYAEQD

FIG.27E



HYDROPHOBIC

LFIEGLYLFTL

RYFYWYTIIGWGTPVCVTW

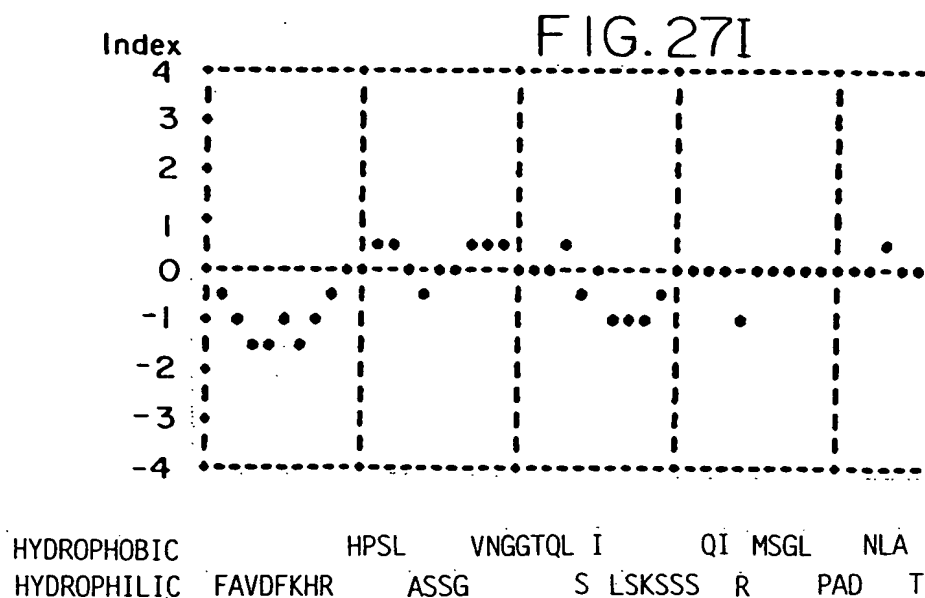
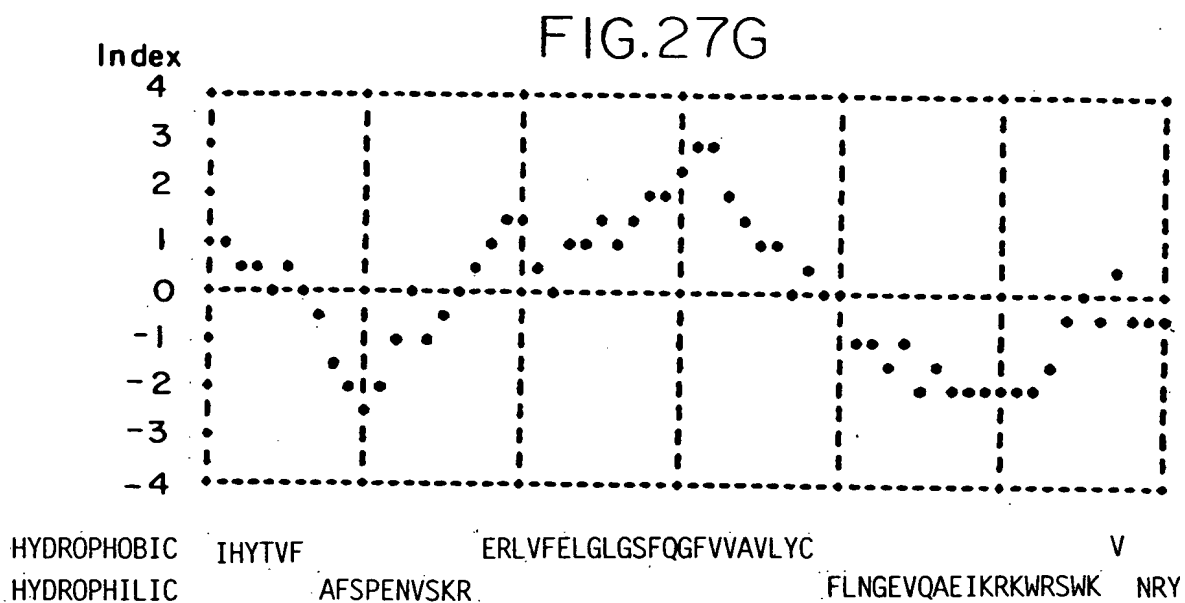
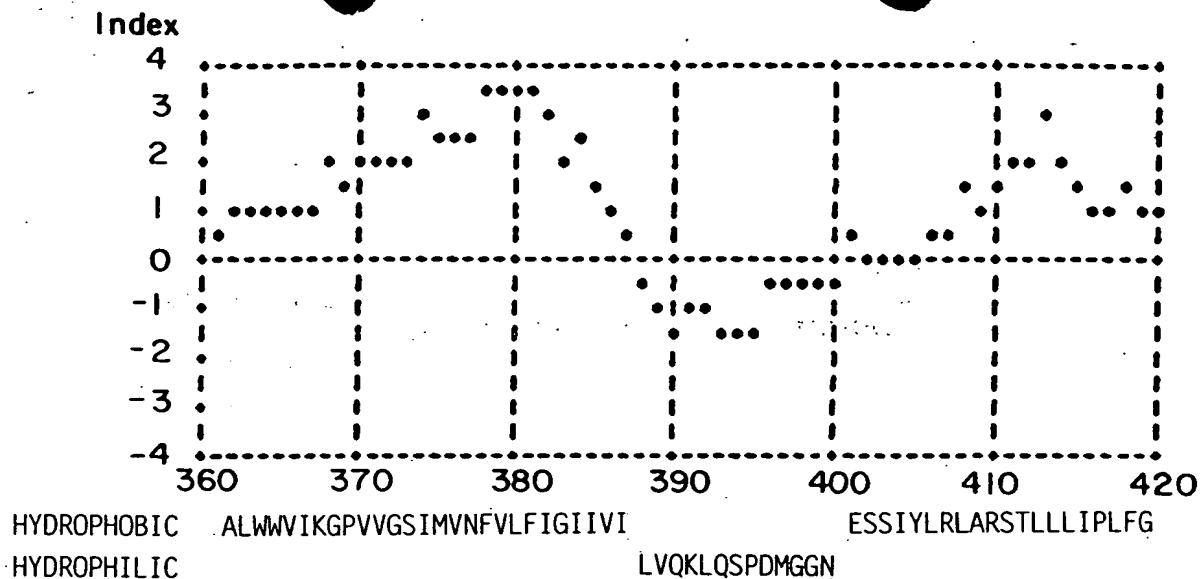
DST

HYDROPHILIC

LVETFFPER

ATRLRYFDDTGCWDMN

FIG.27F



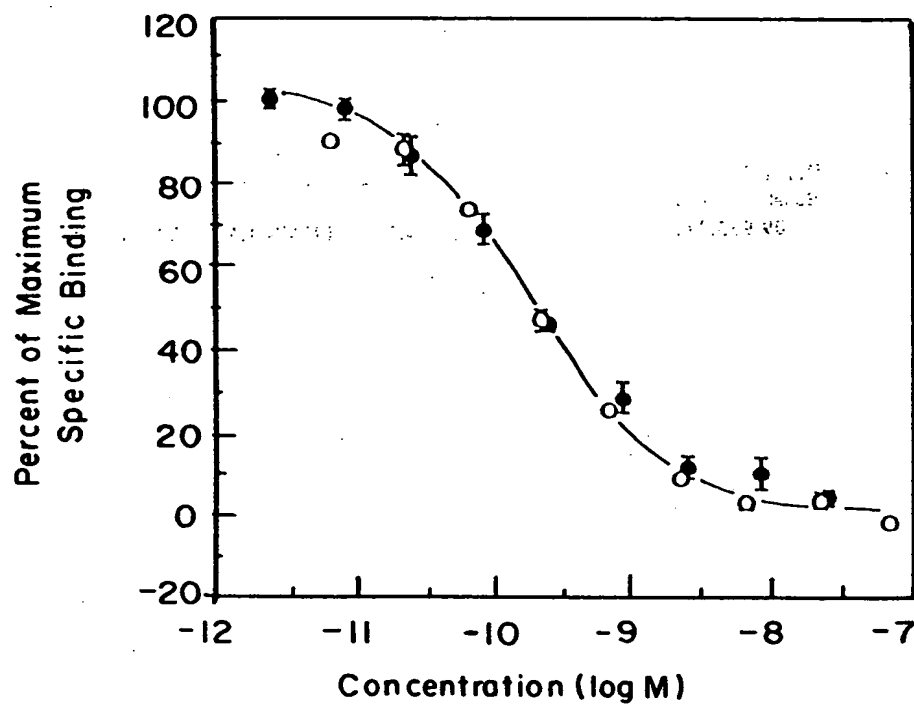


FIG. 29

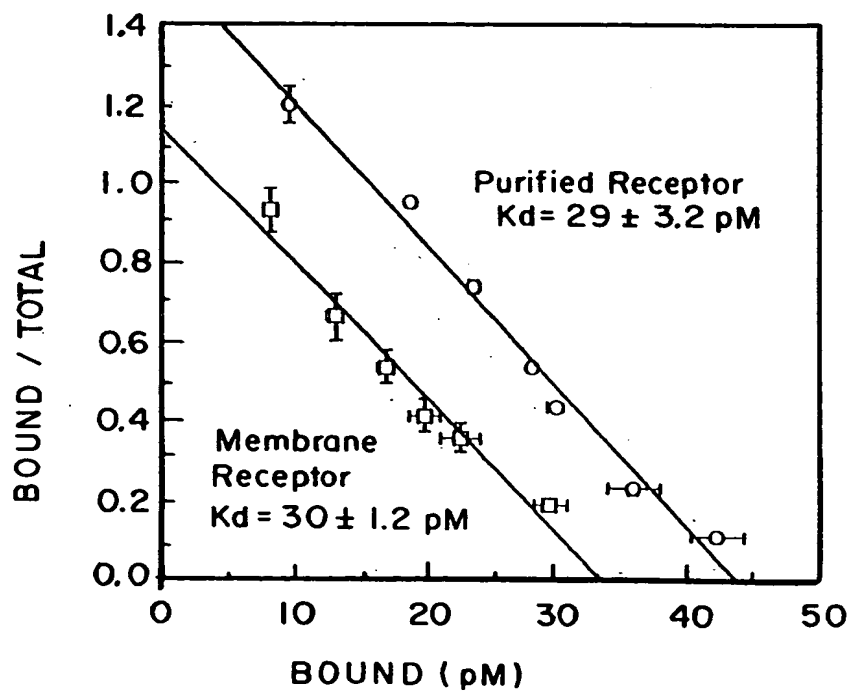


FIG. 30



FIG.31

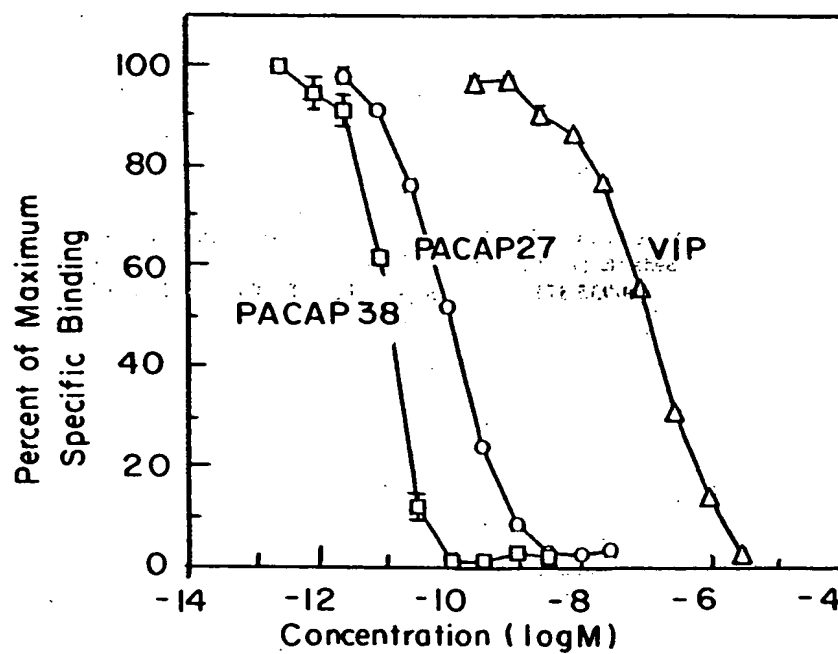


FIG.33

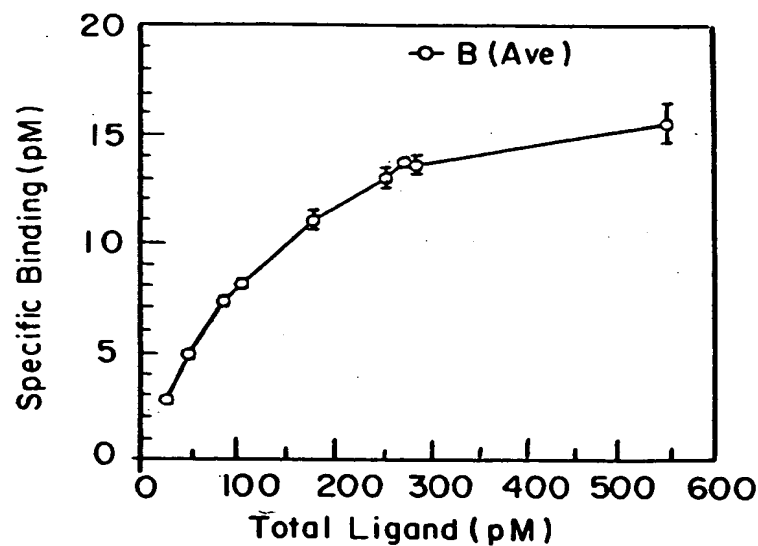


FIG.34

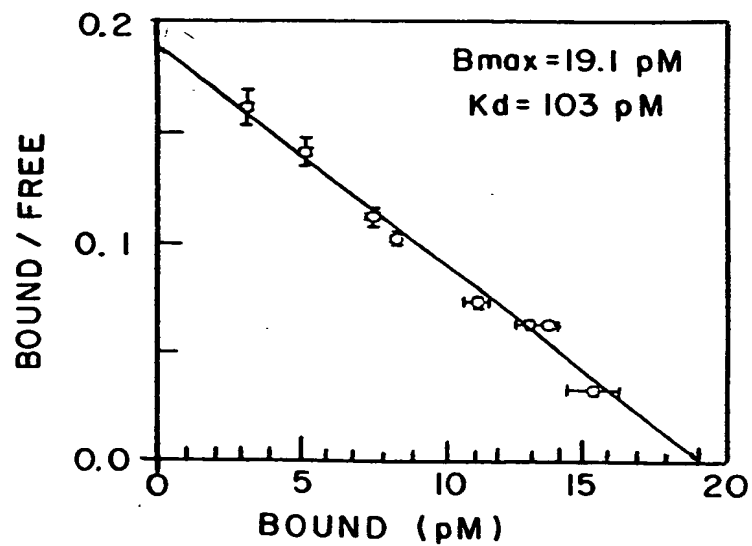


FIG. 35

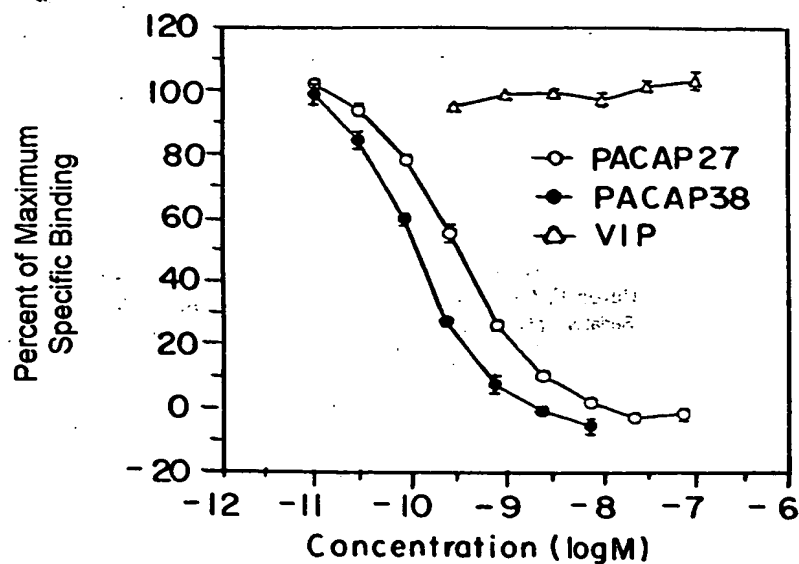


FIG.36

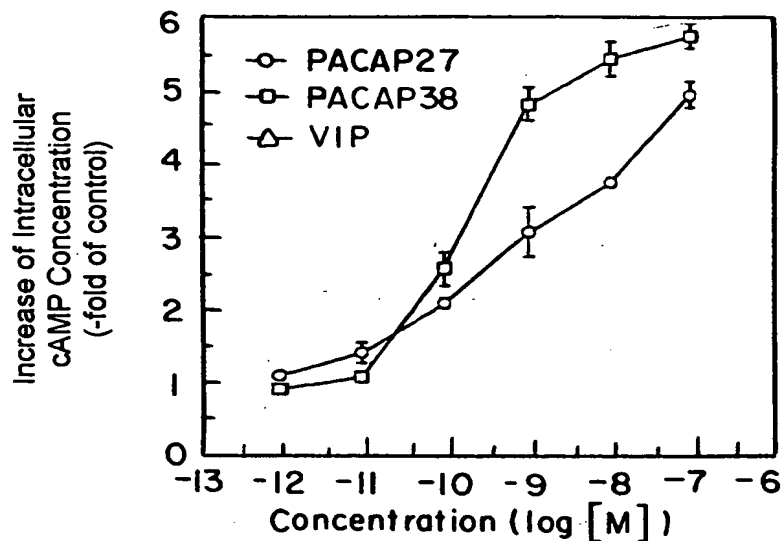


FIG.37

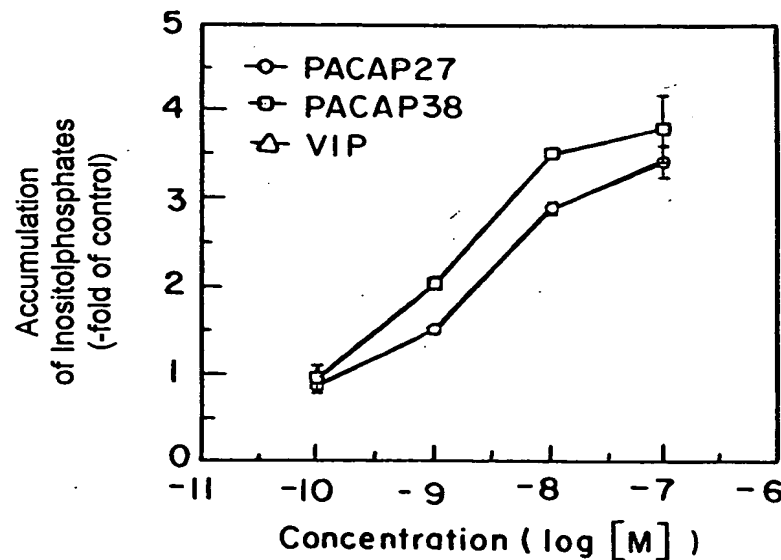


FIG.32

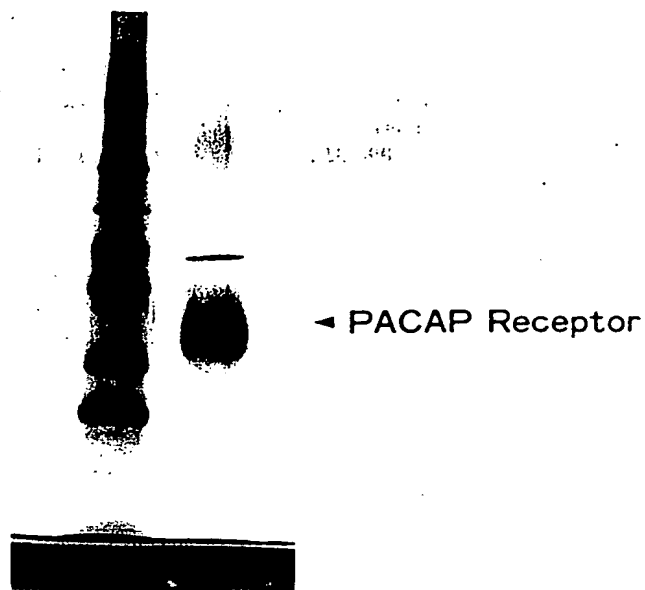


FIG.38

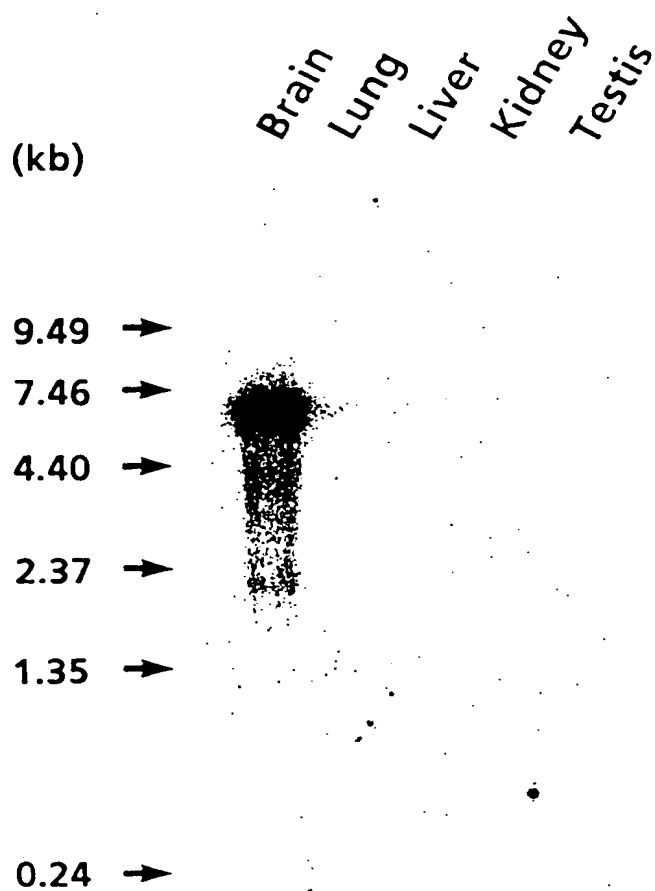


FIG.39

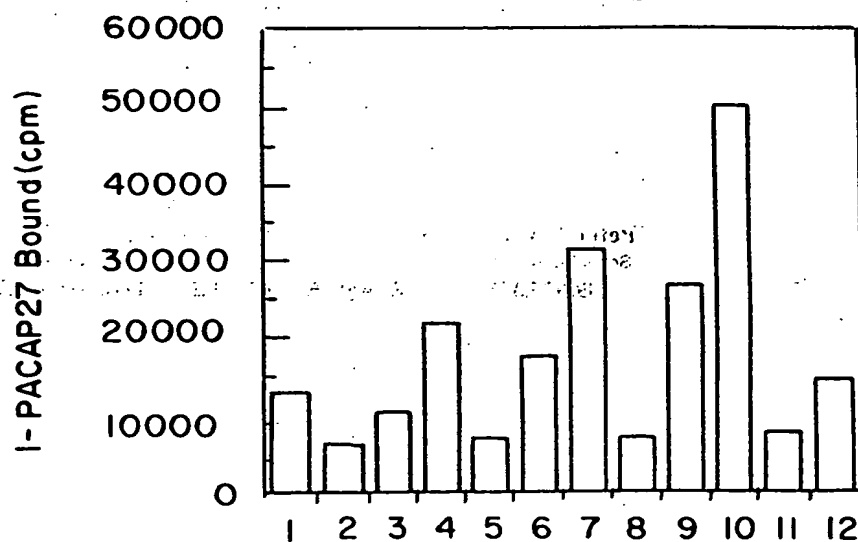


FIG.42

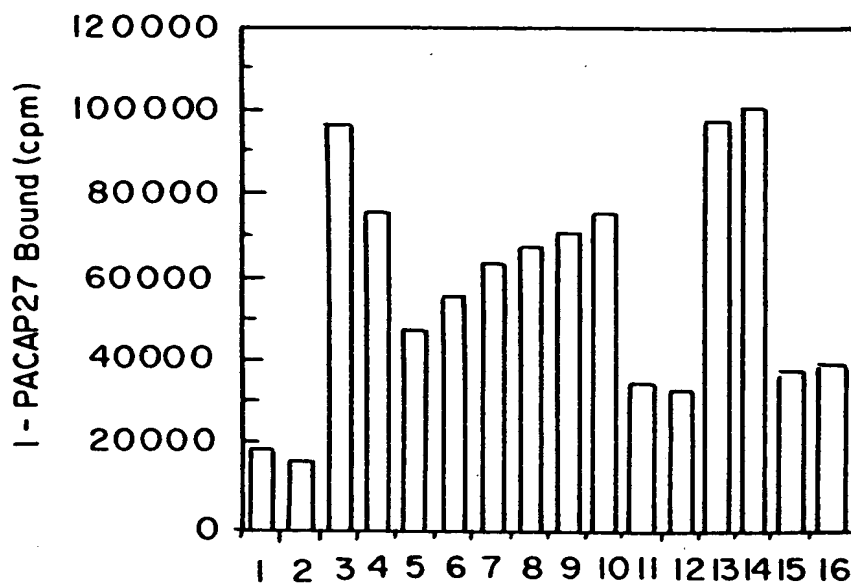
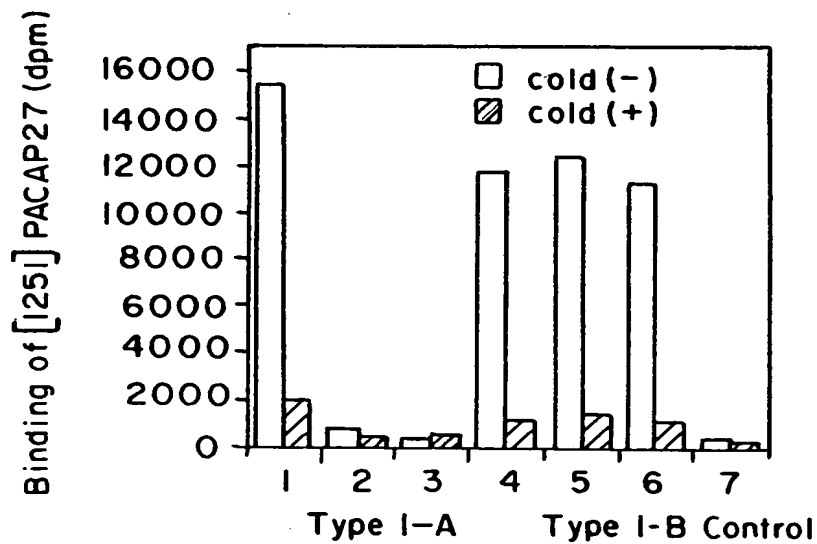


FIG.44



I-PACAP27 Specific Binding ( % of control )

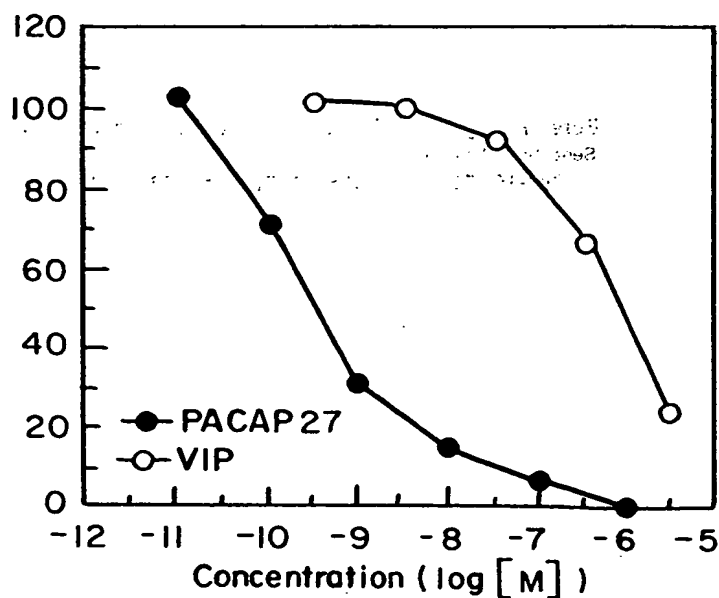


FIG. 40A

I-PACAP27 Specific Binding ( % of control )

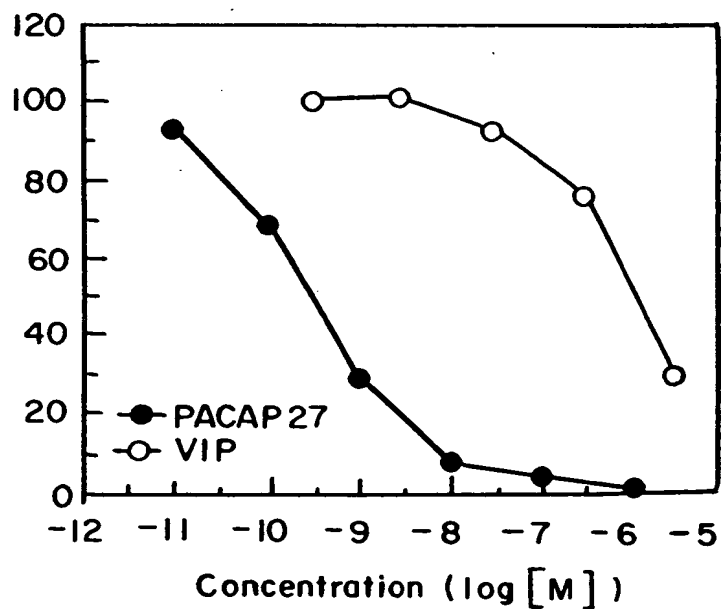


FIG. 40B

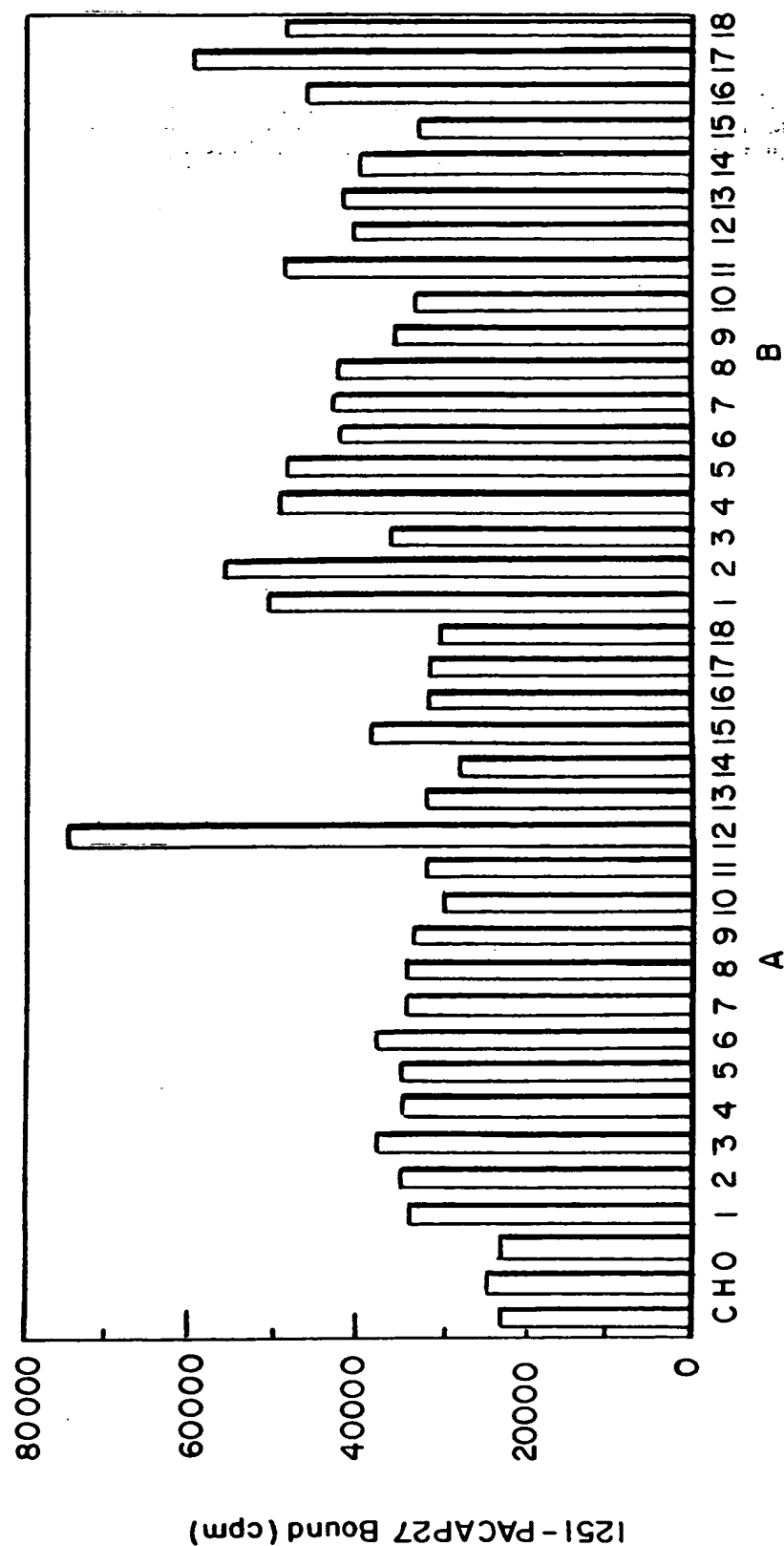


FIG. 41

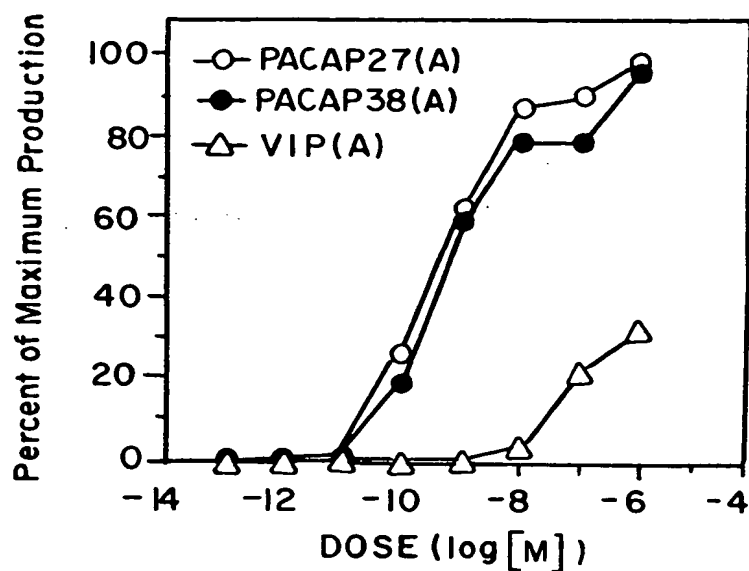


FIG. 43A

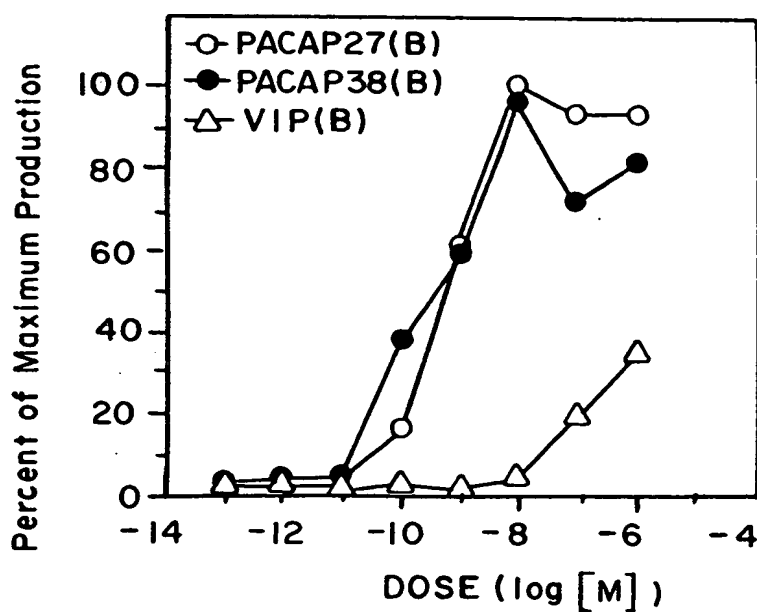


FIG. 43B

125I-PACAP27 Binding

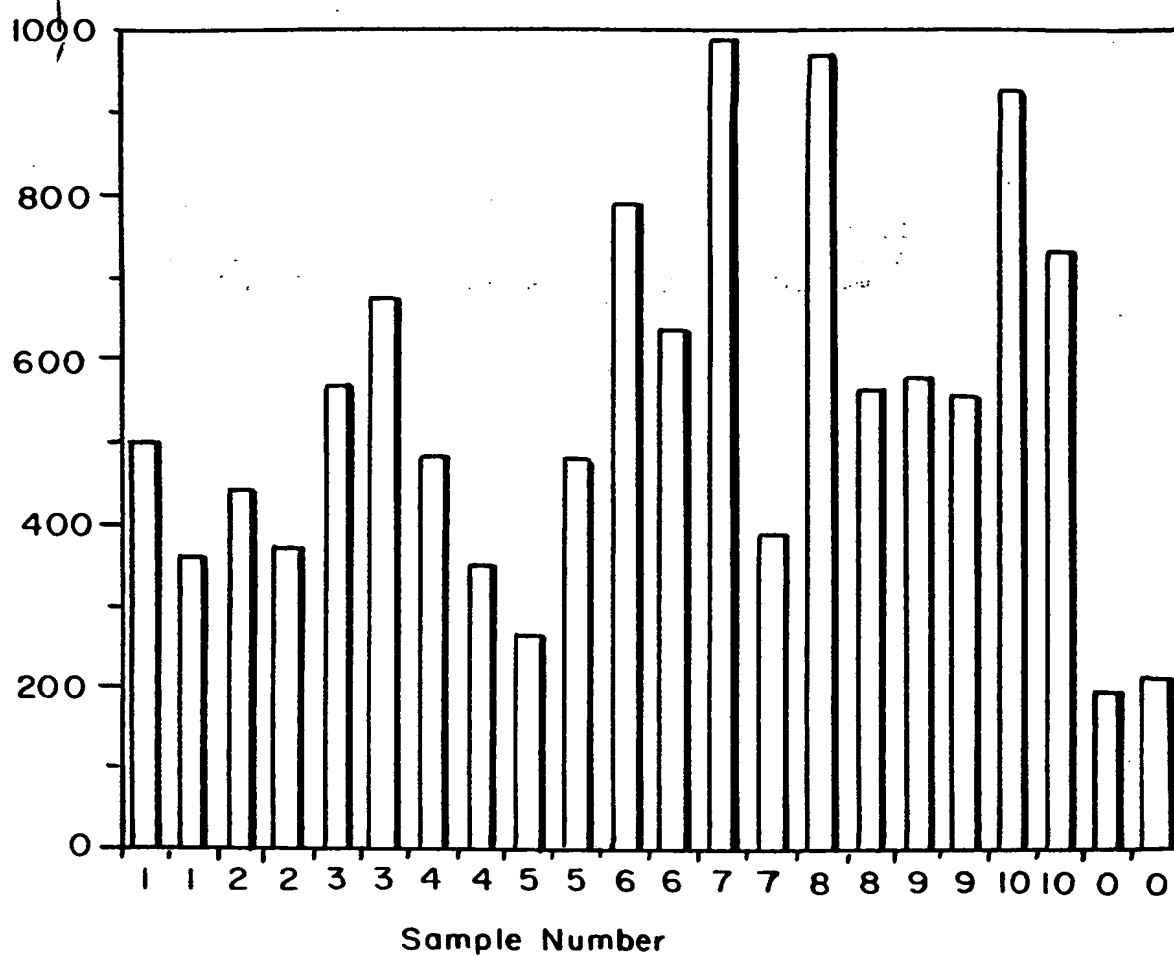


FIG. 45

FIG. 46

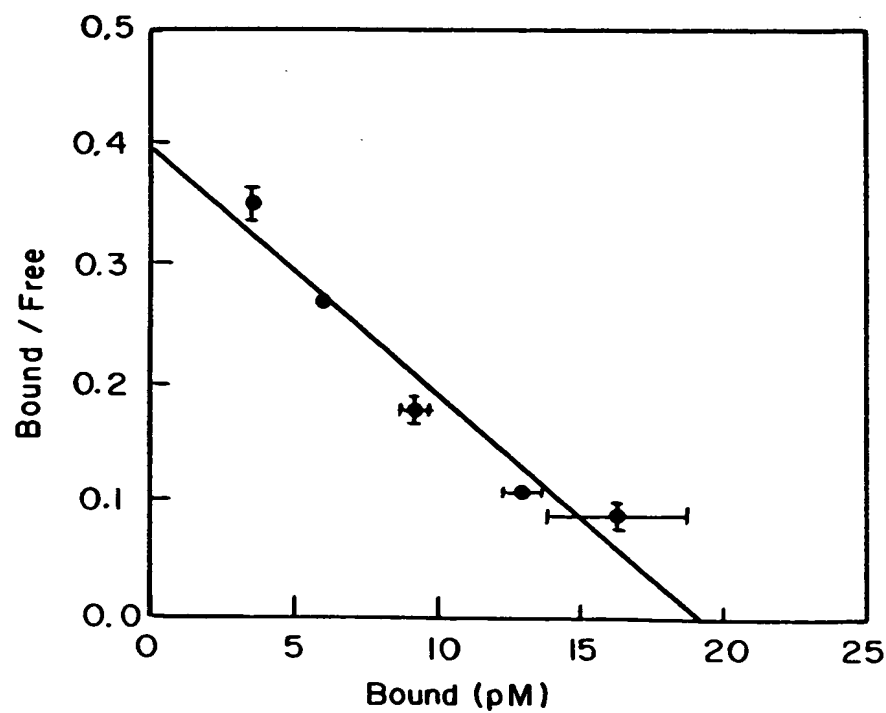




FIG.47

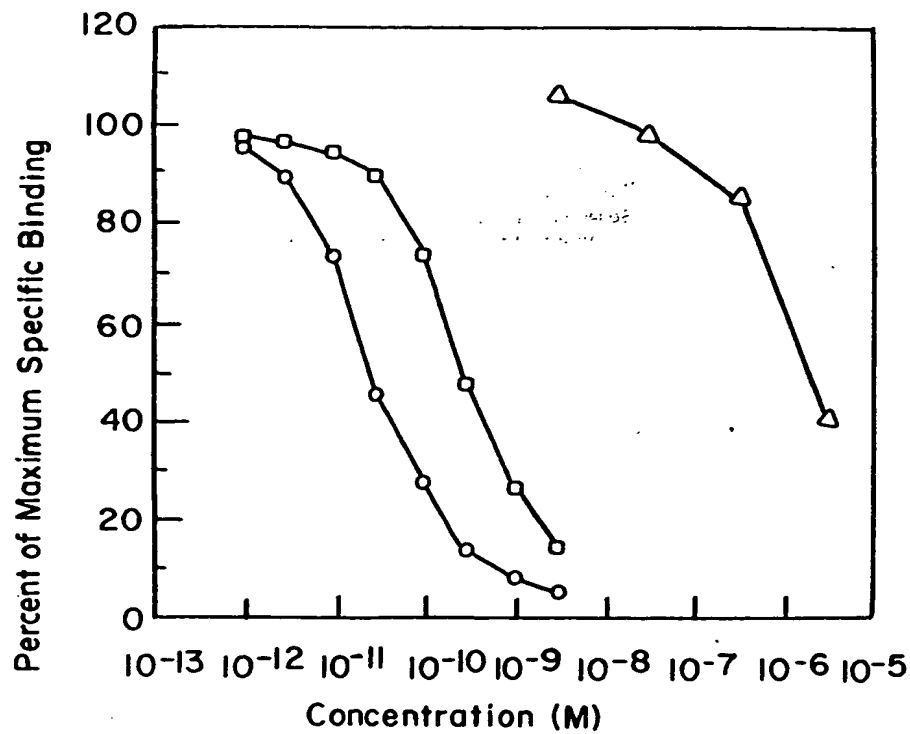
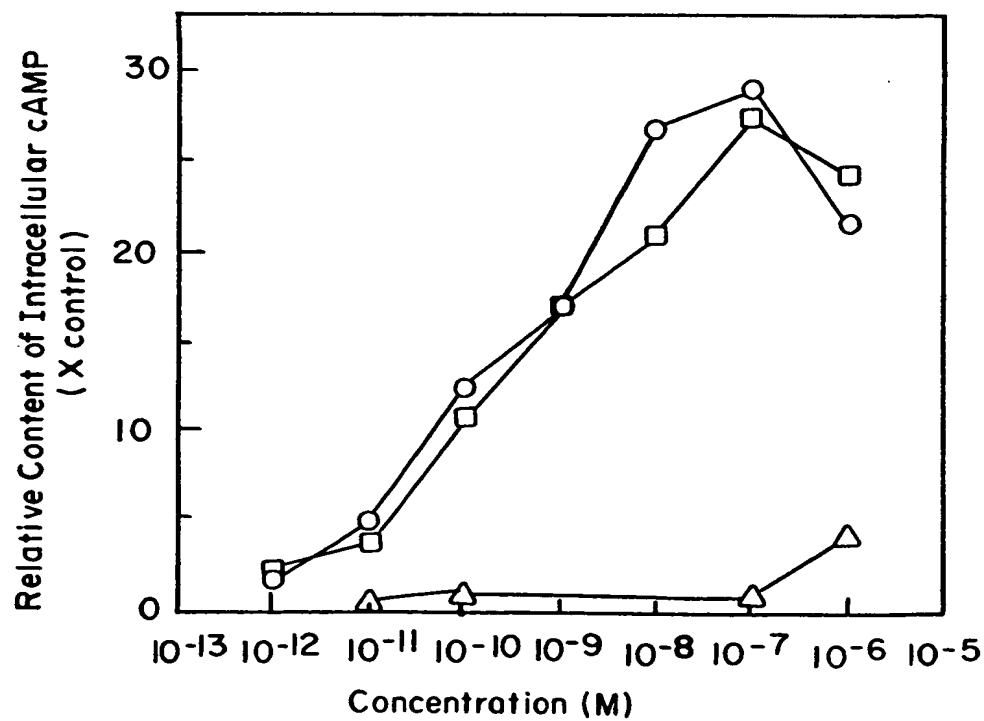


FIG.48



(kb)

Brain  
Lung  
Liver  
Thymus  
Spleen  
Pancreas  
Placenta

9.49

7.46

4.40

2.37

1.35

0.24

(kb)

Olfactory Bulb  
Amygdala  
Basal Ganglia  
Hippocampus  
Thalamus  
Hypothalamus  
Cerebral Cortex  
Medulla  
Cerebellum  
Spinal Cord  
Pituitary

9.49

7.46

4.40

2.37

1.35

0.24

FIG. 49

FIG. 49 shows the results of a Southern blot analysis of DNA from various tissues. The DNA was digested with EcoRI and probed with a cDNA probe. The results show that the probe hybridizes to a single band in all tissues, indicating that the gene is expressed in all tissues.

FIG. 50

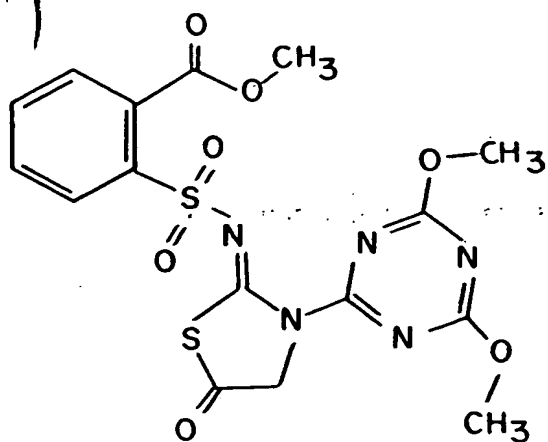


FIG. 5IA

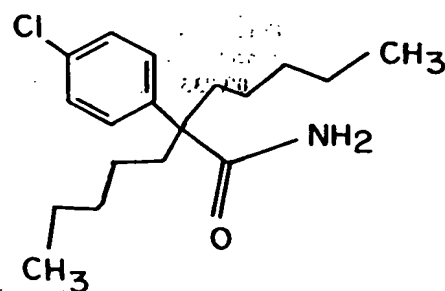


FIG. 5IB

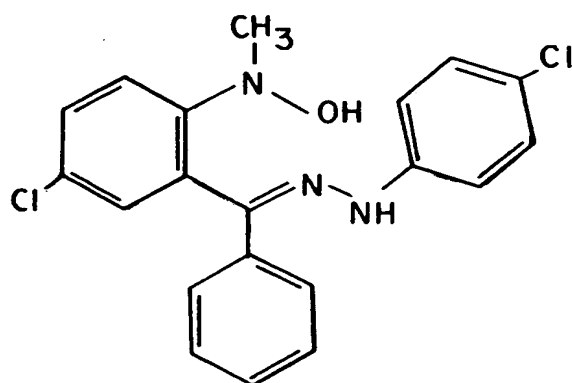


FIG. 5IC

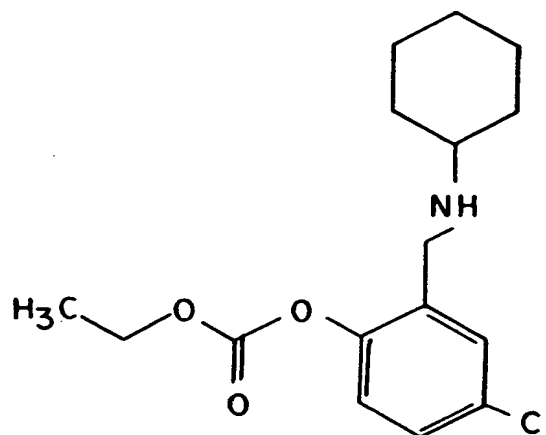


FIG. 5ID

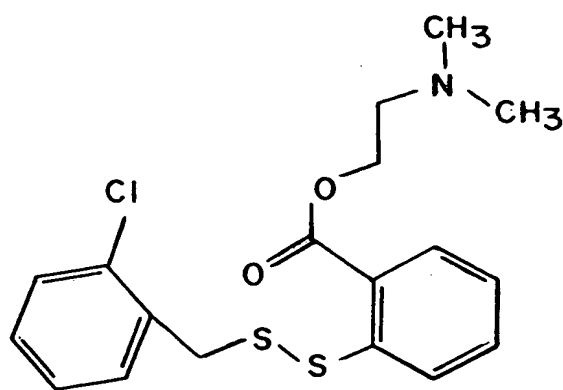


FIG. 5IE

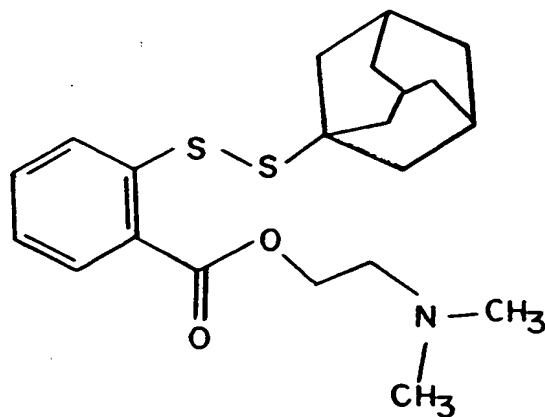


FIG. 5IF

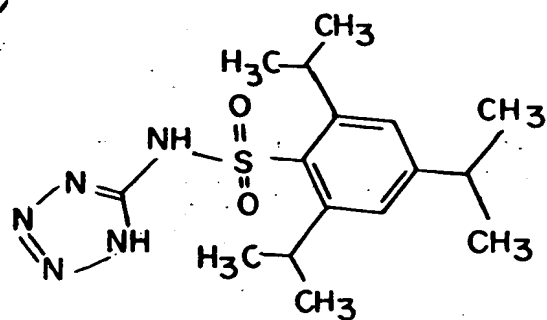


FIG. 5IG

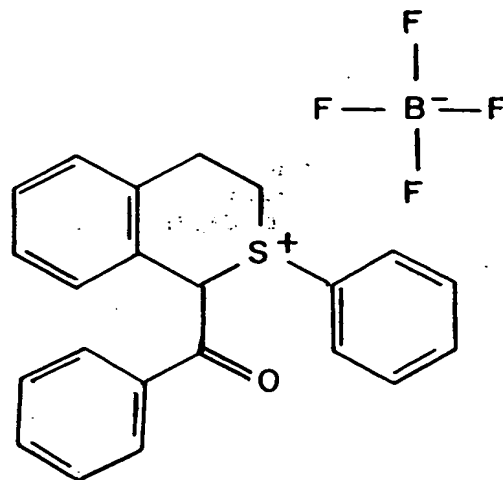


FIG. 5IH

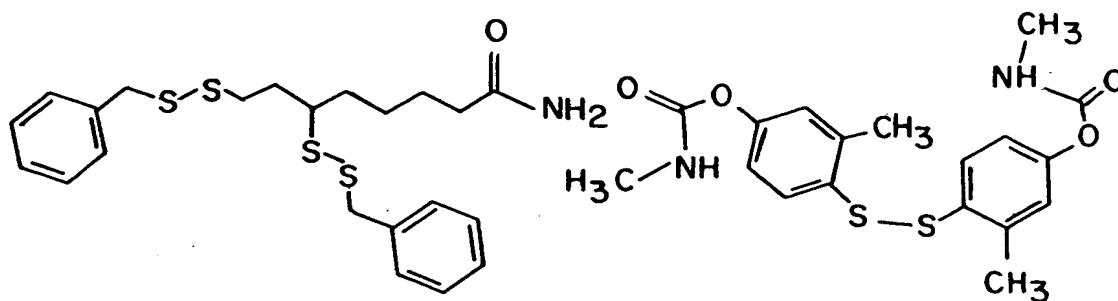


FIG. 5II

FIG. 5IJ

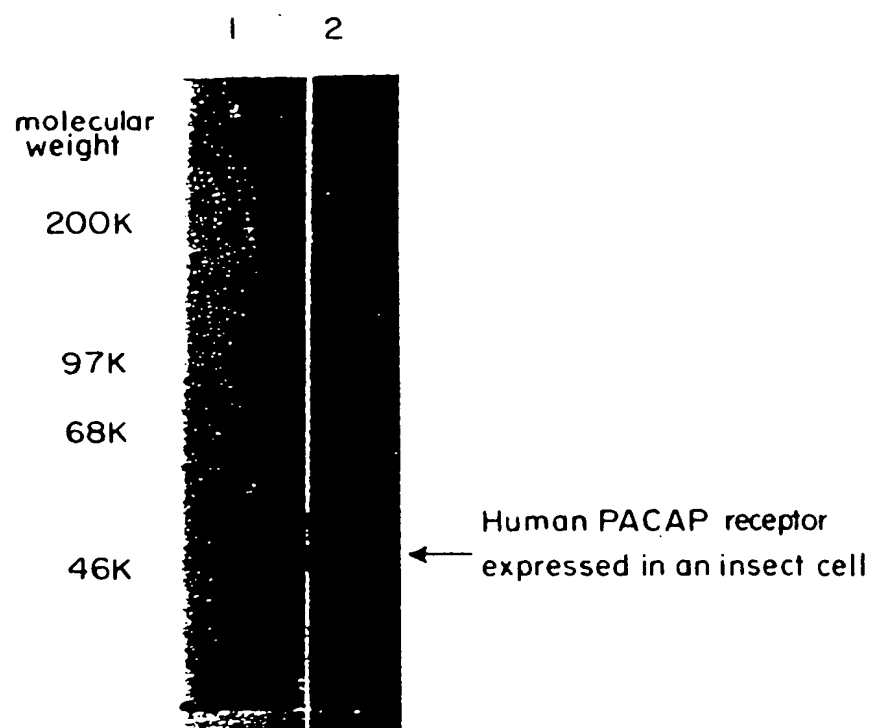


FIG. 53

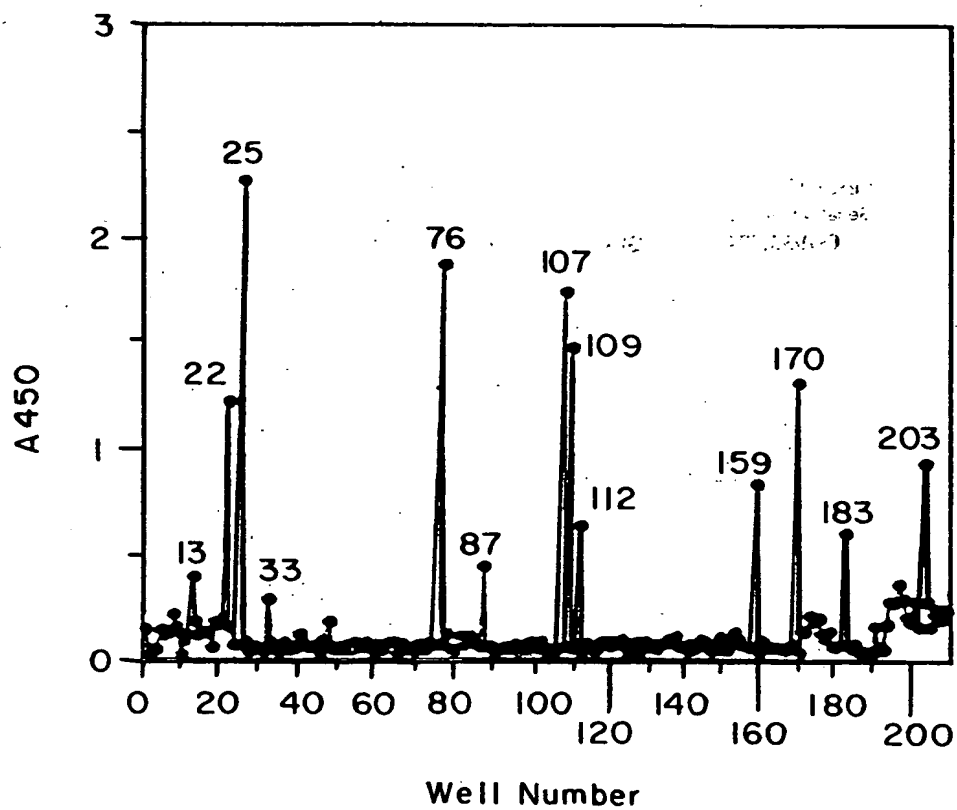


FIG. 52

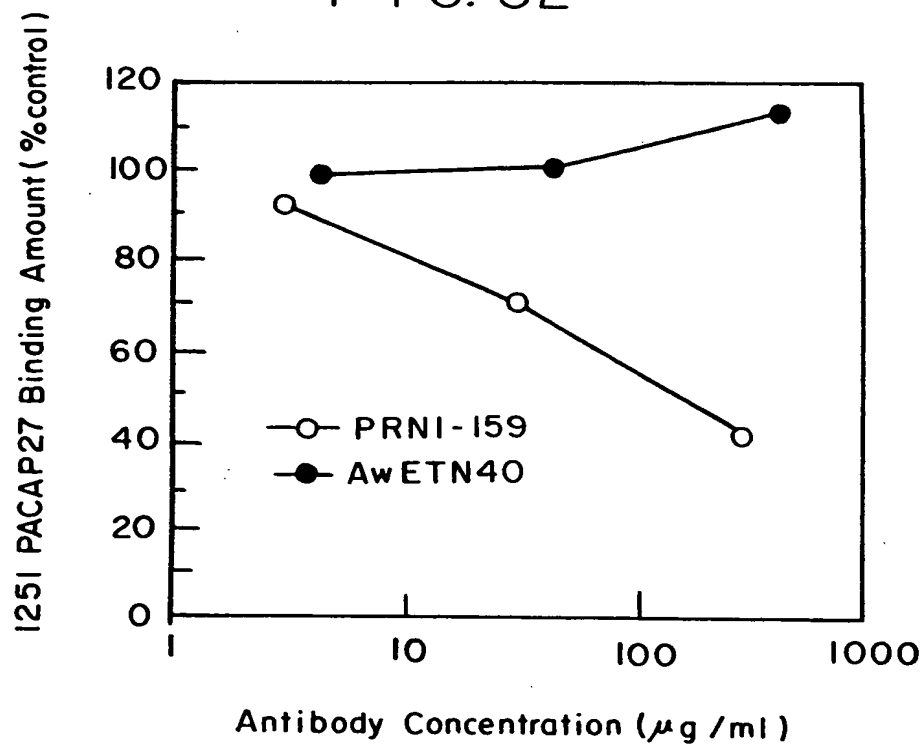


FIG. 54